

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 25, 2006, 18:42:01 ; Search time 71 Seconds
(without alignments)
168.929 Million cell updates/sec

Title: US-10-737-290-172

Perfect score: 92

Sequence: 1 CFGRKMDRISSSGGLGC 17

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	ID	Description
1	92	100.0	134	1 ANFB_HUMAN	P16860 homo sapien
2	92	100.0	134	2 Q6FGY0_HUMAN	Q6FGY0 homo sapien
3	76	82.6	103	1 ANFB_BOVIN	P13204 bos taurus
4	76	82.6	112	2 Q9GLK5_FELCA	Q9GLK5 felis silve
5	76	82.6	126	1 ANFC2_ORYLA	Q8AYR5 oryzias lat
6	76	82.6	129	1 ANFB_SHEEP	Q46541 ovis aries
7	76	82.6	131	1 ANFB_PIG	P07634 sus scrofa
8	76	82.6	132	1 ANFB_FELCA	Q9GLK4 felis silve
9	76	82.6	132	2 Q6L7Z3_CAMDR	Q6L7Z3 camelus dro
10	76	82.6	140	1 ANFB_CANFA	P16859 canis fami
11	76	82.6	146	2 Q7T2I7_ONCMY	Q7T2I7 oncorhynch
12	76	82.6	148	2 Q78AW6_SALSA	Q78AW6 salmo salar
13	76	82.6	152	2 Q9YJG7_SALSA	Q9YJG7 salmo salar
14	74	80.4	37	1 NFNP_PSEPC	P82972 pseudoceras
15	74	80.4	38	2 Q7LZ09_VIPLE	Q7LZ09 vipera lebe
16	74	80.4	83	2 Q4TD23_TETNG	Q4TD23 tetraodon n
17	74	80.4	133	1 ANFB_FUGRU	Q805d7 fugu rubrip
18	74	80.4	138	1 ANFB_OREMO	Q805e8 oreochromis
19	74	80.4	146	2 Q7TIQ2_ORYLA	Q7TIQ2 oryzias lat
20	74	80.4	150	1 ANFC_ACITR	Q76KW6 acipenser t
21	74	80.4	162	2 Q7YU55_EPTBU	Q7YU55 eptatretus
22	73	79.3	25	2 Q4SND6_TETNG	Q4SND6 tetraodon n
23	73	79.3	33	2 Q9QZ96_CAVPO	Q9QZ96 cavia porce
24	73	79.3	126	1 ANFC1_FUGRU	Q805d6 fugu rubrip
25	73	79.3	126	1 ANFC_BOVIN	P55206 bos taurus
26	73	79.3	126	1 ANFC_HUMAN	P23582 homo sapien
27	73	79.3	126	1 ANFC_PIG	Q61839 mus musculu
28	73	79.3	126	1 ANFC_PIG	P18104 mus musculu
29	73	79.3	126	1 ANFC_RAT	P55207 rattus norv
30	73	79.3	126	1 ANFC_SHEEP	P56283 ovis aries
31	73	79.3	126	2 Q4ZG41_HUMAN	Q4ZG41 homo sapien

32	73	79.3	126	2 Q544K5_MOUSE	Q544K5 mus musculu
33	73	79.3	131	1 ANFC1_ONCMY	Q8AXR3 oncorhynch
34	73	79.3	131	1 ANFC1_ORYLA	Q8AYR6 oryzias lat
35	73	79.3	131	1 ANFC2_ONCMY	Q8AXR2 oncorhynch
36	73	79.3	131	2 Q805E7_OREMO	Q805e7 oreochromis
37	73	79.3	137	2 Q5Y820_XENLA	Q5Y820 xenopus lae
38	73	79.3	138	2 Q4T953_TETNG	Q4T953 tetraodon n
39	73	79.3	139	1 ANFB_FUGRU	Q805d8 fugu rubrip
40	73	79.3	140	1 ANFB_CHICK	P18908 gallus gall
41	73	79.3	140	1 ANFB_OREMO	Q805e9 oreochromis
42	73	79.3	147	2 Q8VHG9_TOTAL	Q8VHG9 notomys ale
43	73	79.3	181	2 Q90Y11_CRODU	Q90Y11 crotalus du
44	73	79.3	181	2 Q90Y12_CRODU	Q90Y12 crotalus du
45	72	78.3	22	1 ANFC_CHICK	P21805 gallus gall
46	72	78.3	27	1 ANFC_ANGJA	P18144 anguilla ja
47	72	78.3	101	2 Q4S797_TETNG	Q4S797 tetraodon n
48	72	78.3	120	1 ANFC4_FUGRU	Q805d3 fugu rubrip
49	72	78.3	121	1 ANFC4_ORYLA	Q805i7 oryzias lat
50	72	78.3	130	1 ANFC2_FUGRU	Q805d5 fugu rubrip
51	72	78.3	131	1 ANFC_ANGJA	P18145 anguilla ja
52	72	78.3	140	2 Q9PSV1_ANGJA	Q9PSV1 anguilla ja
53	72	78.3	150	1 ANFB_ANGJA	P22642 anguilla ja
54	72	78.3	277	2 Q4TBD2_TETNG	Q4TBD2 tetraodon n
55	71	77.2	149	1 ANFB_CANFA	P07499 canis fami
56	71	77.2	150	1 ANFB_ACITR	P83965 acipenser t
57	71	77.2	150	1 ANFB_PIG	P24259 sus scrofa
58	71	77.2	151	2 Q5JZE1_HUMAN	Q5JZE1 homo sapien
59	71	77.2	152	1 ANFB_BOVIN	P07501 bos taurus
60	71	77.2	152	1 ANFB_SHEEP	Q46540 ovis aries
61	71	77.2	152	2 Q6L7Z4_CAMDR	Q6L7Z4 camelus dro
62	71	77.2	152	2 Q9TQW1_BALPH	Q9TQW1 balaeopter
63	71	77.2	153	1 ANFB_FELCA	Q9GID0 felis silve
64	71	77.2	153	1 ANFB_HORSE	P27104 equus cabal
65	71	77.2	153	1 ANFB_HUMAN	P01160 homo sapien
66	71	77.2	155	2 Q29130_TUPGB	Q29130 tupaia glis
67	70	76.1	118	1 ANFD_RANCA	P40756 rana cateeb
68	70	76.1	135	1 ANFC_SQUAC	P41319 squalus aca
69	70	76.1	144	2 Q805E6_FUNHE	Q805e6 fundulus he
70	70	76.1	221	2 Q7TIM4_BOTJR	Q7TIM4 bothrops ja
71	70	76.1	256	2 Q6LEM5_BOTJA	Q6LEM5 bothrops ja
72	70	76.1	263	2 Q9PT52_AKGHA	Q9PT52 agkistrodon
73	70	76.1	265	2 Q8QG91_BOTIN	Q8QG91 bothrops in
74	69	75.0	115	1 ANFC_SCYCA	P23259 scyllorhinu
75	69	75.0	136	1 ANFC_TRISC	P55208 triakis scy
76	69	75.0	265	2 Q9PW56_BOTJA	Q9PW56 bothrops ja
77	68	73.9	129	1 ANFC_RANCA	P20968 rana cateeb
78	67	72.8	106	2 Q6VYM3_BRARE	Q6VYM3 brachydano
79	67	72.8	152	1 ANFB_MOUSE	P05125 mus musculu
80	67	72.8	152	1 ANFB_RAT	P01161 rattus norv
81	67	72.8	152	2 Q5FW59_MOUSE	Q5FW59 mus musculu
82	67	72.8	152	2 Q8VHH2_NOTAL	Q8VHH2 notomys ale
83	67	72.8	153	1 ANFB_RABIT	P07500 oryctolagus
84	66	71.7	30	1 ANFB_RANRI	P09196 rana ridibu
85	66	71.7	104	2 Q6DF98_XENLA	Q6DF98 xenopus lae
86	66	71.7	145	1 ANFB_RANCA	P18909 rana cateeb
87	66	71.7	145	2 Q5XPR8_RANRI	Q5XPR8 rana ridibu
88	66	71.7	159	2 Q90XG1_BUFMA	Q90XG1 bufo marinu
89	65	70.7	35	2 Q8PRU2_ONCMY	Q8PRU2 oncorhynch
90	65	70.7	39	1 VNOC_OXYMI	P83230 oxyuranus m
91	65	70.7	39	1 VNOC_OXYSA	P83231 oxyuranus s
92	65	70.7	121	1 ANFB_MOUSE	P40753 mus musculu
93	65	70.7	121	2 Q794A8_MOUSE	Q794A8 mus musculu
94	65	70.7	121	2 Q91V40_MUSSI	Q91V40 mus spicile
95	65	70.7	121	2 Q54AE9_MOUSE	Q54AE9 mus musculu
96	65	70.7	121	2 Q55086_MOUSE	Q55086 mus musculu
97	65	70.7	128	1 ANFB_CAVPO	P27596 cavia porce
98	65	70.7	139	2 P79799_MICCO	P79799 micrurus co
99	65	70.7	147	2 Q9DGR8_XENLA	Q9DGR8 xenopus lae
100	65	70.7	149	2 Q7T2I6_ONCMY	Q7T2I6 oncorhynch
101	64	69.6	112	1 ANFC3_ORYLA	Q800i8 oryzias lat
102	63	68.5	38	1 DNP_DENAN	P28374 dendroaspis
103	63	68.5	53	2 Q8QGP7_DENAN	Q8QGP7 dendroaspis
104	63	68.5	121	1 ANFB_RAT	P13205 rattus norv

105	62	67.4	111	2	Q8HXV3_SAGOE	Q8bxv3	seguinus oe	178	41	44.6	183	2	Q9LK59_ARATH	Q9lk59	arabidopsis
106	62	67.4	111	2	Q8HXV4_9PRIM	Q8bxv4	macaca sp.	179	41	44.6	231	2	Q8KBV3_CHLTE	Q8kbv3	chlorobium
107	62	67.4	111	2	Q8HXV5_PONPY	Q8bxv5	pongo pygma	180	41	44.6	307	1	SPT3_SCHPO	O14311	schizosacch
108	62	67.4	111	2	Q8HXV6_9PRIM	Q8bxv6	gorilla gor	181	41	44.6	314	2	Q4J243_AZQVI	Q4j243	azotobacter
109	62	67.4	111	2	Q8HXV7_PANTR	Q8bxv7	pan troglod	182	41	44.6	327	2	Q81GC1_BACCR	Q81gc1	bacillus ce
110	62	67.4	142	1	ANF_ACTIR	P83964	acipenser t	183	41	44.6	338	2	Q63U31_BURPS	Q63u31	burkholderi
111	61	66.3	35	1	VNOA_OXYMI	P83224	oxyuranus m	184	41	44.6	338	2	Q62K99_BURMA	Q62k99	burkholderi
112	61	66.3	35	1	VNOA_OXYSC	P83226	oxyuranus s	185	41	44.6	366	2	Q75HQ9_ORYSA	Q75hq9	oryza sativ
113	61	66.3	35	1	VNOA_OXYSC	P83225	oxyuranus s	186	41	44.6	441	2	Q20533_9EURO	O20533	ascosphaera
114	61	66.3	35	1	VNOB_OXYMI	P83227	oxyuranus m	187	41	44.6	523	2	Q92YU3_RHIME	Q92yu3	rhizobium m
115	61	66.3	35	1	VNOB_OXYSC	P83229	oxyuranus s	188	41	44.6	620	2	Q80SZ6_MOUSE	Q80sz6	mus musculus
116	61	66.3	35	1	VNOB_OXYSC	P83228	oxyuranus s	189	41	44.6	650	2	Q58EJ8_BRARE	Q58ej8	brachydanio
117	61	66.3	111	2	Q4VR12_OXYSC	Q4vr12	oxyuranus s	190	41	44.6	681	2	Q7ZZ29_BRARE	Q7zz29	brachydanio
118	60	65.2	128	2	Q4T954_TETNG	Q4t954	tetraodon n	191	41	44.6	738	2	Q9A3Z5_CAUCR	Q9a3z5	caulobacter
119	60	65.2	158	1	ANFC3_FUGRU	Q805d4	fugu rubrip	192	41	44.6	745	2	Q6CVJ4_KULJA	Q6cvj4	kluveromyc
120	59	64.1	145	1	ANFV_ACTR	P83962	acipenser t	193	41	44.6	746	2	Q92457_TIRE	Q92457	trichoderma
121	56	60.9	126	2	Q9D288_MOUSE	Q9d288	mus musculus	194	41	44.6	757	2	Q928E8_LIFIN	Q928e8	listeria in
122	51	55.4	420	2	Q7UNAG_RHOBA	Q7una6	rhodopirell	195	41	44.6	797	2	Q9HXV4_PSEAE	Q9hxy4	pseudomonas
123	44	52.2	883	2	Q9LDG7_ARATH	Q9ldg7	arabidopsis	196	41	44.6	914	1	GUX2_CLOSR	P50900	clostridium
124	46	50.0	407	1	PRGR_RANDY	Q7xzt1	xenopus lae	197	41	44.6	946	2	Q5CX18_CHYPV	O5cx18	cryptospori
125	46	50.0	711	1	Q4WB57_ASPFU	Q4wb57	aspergillus	198	41	44.6	999	2	Q4QSS1_LEIMA	Q4qss1	leishmania
126	46	50.0	723	2	Q7N6B2_PHOLL	Q7n6b2	photorhabd	199	41	44.6	1586	2	Q5JPZ2_ORYSA	Q5jpz2	oryza sativ
127	45	49.5	265	2	Q9GLD8_FELCA	Q9glid8	felis silve	200	41	44.6	2523	2	Q61211_CAEBR	Q61211	caenorhabdi
128	45	48.9	33	2	Q75JA9_DICDI	Q75ja9	dictyosteli	201	40.5	44.0	292	2	Q4NX98_9DELT	Q4nxx98	anaeromyxob
129	45	48.9	381	2	Q55AQ3_DICDI	Q55aq3	dictyosteli	202	40.5	44.0	970	2	Q80790_ARATH	Q80790	arabidopsis
130	45	48.9	381	2	C08B_PAROL	Q9pww7	paralichthy	203	40	43.5	53	2	Q8CLV0_YERPE	O8clv0	versinia pe
131	44.5	48.4	588	1	Q4ZX16_PSESY	Q4zx16	pseudomonas	204	40	43.5	61	2	Q8NHLV_FRATT	Q8nlv0	francisella
132	44	47.8	145	2	Q8GVG8_ARATH	Q8gv88	arabidopsis	205	40	43.5	116	2	Q8NDLJ8_SNYEL	Q8ndl8	synecococc
133	44	47.8	226	2	Q8REVI_TETNG	Q8rev1	tetraodon n	206	40	43.5	152	2	Q7RUFO_NEUCR	Q7ruf0	neurospora
134	44	47.8	496	2	Q8YURI_BROME	Q8yuri	brucella me	207	40	43.5	163	2	Q28954_PIG	Q28954	sus scrofa
135	44	47.8	533	2	Q8FY42_BRUSU	Q8fy42	brucella su	208	40	43.5	184	2	Q6S8Z8_PLAFA	O6s8z8	plasmodium
136	44	47.8	533	2	Q98H36_RHILLO	Q98h36	rhizobium l	209	40	43.5	223	2	Q7UM83_RHOBA	Q7um83	rhodopirell
137	44	47.8	540	2	Q92KZ4_RHIME	Q92kz4	rhizobium m	210	40	43.5	247	2	Q6YXH7_ORYSA	Q6yxh7	oryza sativ
138	44	47.8	740	2	Q5Z8V2_ORYSA	Q5z8v2	oryza sativ	211	40	43.5	267	2	Q7HFP0_COLGL	Q7hfp0	colletotric
139	44	47.8	740	2	Q8IEU9_PLAF7	O8ieu9	plasmodium	212	40	43.5	272	1	KSGA_GLOVI	Q9ajl9	g dimethyla
140	44	47.8	3346	2	Q6YZB8_ORYSA	Q6yzb8	oryza sativ	213	40	43.5	295	2	Q9AJL9_HYDTH	Q9ajl9	hydrogenoba
141	43	46.7	161	2	Q9FVZ8_ARATH	Q9fvz8	arabidopsis	214	40	43.5	298	1	MCES_ENCCU	O8ar66	encephalito
142	43	46.7	166	2	Q9FWM2_ARATH	Q9fwm2	arabidopsis	215	40	43.5	302	2	Q704A7_THETE	Q704a7	thermoprote
143	43	46.7	182	2	Q6NLT6_ARATH	O6nlit6	arabidopsis	216	40	43.5	340	2	Q49UJ6_FIGES	O49uv4	caenorhabdi
144	43	46.7	231	2	Q9FX12_ARATH	O9fx12	arabidopsis	217	40	43.5	358	2	O57588_FUGRU	O57588	fugu rubrip
145	43	46.7	325	2	Q6FRI8_CANGA	O6fri8	candida gla	218	40	43.5	379	2	Q5YPU6_NOCFA	O5ypu6	nocardia fa
146	43	46.7	436	2	Q5CNT5_CRYHO	O5cnt5	cryptospori	219	40	43.5	396	2	Q7VTD8_BORPE	Q7vtd8	bordetella
147	43	46.7	522	2	Q22042_CABEL	Q22042	caenorhabdi	220	40	43.5	396	2	Q7WC88_BORPA	O7wc88	bordetella
148	43	46.7	747	1	AGALC_ASPNG	Q9uuz4	aspergillus	221	40	43.5	399	2	Q7WQ92_BORBR	O7wq92	bordetella
149	43	46.7	1045	2	Q4TBW9_TETNG	Q4tbw9	tetraodon n	222	40	43.5	399	2	Q8ZQC6_STRAW	Q8zqc6	streptomyce
150	42.5	46.2	525	2	Q4RLN7_TETNG	Q4rln7	tetraodon n	223	40	43.5	426	2	Q7AUI5_ACTLG	Q7au15	acinetobact
151	42	45.7	196	2	Q9ZNF1_ECOLI	Q9znf1	escherichia	224	40	43.5	468	2	Q4RSU7_TETNG	Q4rsu7	tetraodon n
152	42	45.7	289	2	Q9LS14_ARATH	Q9ls14	arabidopsis	225	40	43.5	481	2	Q60UV4_CAEBR	O60uv4	caenorhabdi
153	42	45.7	273	2	Q25312_HELPY	O25312	helicobacte	226	40	43.5	494	2	O51TS8_MAGGR	O51ts8	magnaporthie
154	42	45.7	273	2	Q9ZLP0_HELPJ	O9zlp0	helicobacte	227	40	43.5	578	2	O5B7X8_EMENI	O5b7x8	aspergillus
155	42	45.7	274	2	Q68229_HELPY	O68229	helicobacte	228	40	43.5	629	2	Q63NX0_BURPS	O63nx0	burkholderi
156	42	45.7	326	2	Q9J1B3_9REOV	Q9j1b3	avian reovi	229	40	43.5	629	2	Q62A37_BURMA	Q62a37	burkholderi
157	42	45.7	433	2	Q4P883_USTWA	Q4p883	ustilago ma	230	40	43.5	637	2	Q5LI52_BACFN	O5li52	bacteroides
158	42	45.7	434	2	Q8LCL1_ARATH	O8lcl1	arabidopsis	231	40	43.5	637	2	Q64Z57_BACFN	O64z57	bacteroides
159	42	45.7	436	2	Q9LFV3_ARATH	Q9lfv3	arabidopsis	232	40	43.5	652	2	Q6CEU2_YARLI	O6ceu2	yarrowia li
160	42	45.7	436	2	Q570M6_ARATH	Q570m6	arabidopsis	233	40	43.5	664	2	Q6P1D1_MOUSE	O6pid1	mus musculus
161	42	45.7	481	2	Q6NCR3_RHOBA	O6ncr3	rhodopseudo	234	40	43.5	705	1	PL01_SCHPO	P50528	schizosacch
162	42	45.7	523	2	Q8PB24_ECOL6	O8pb24	escherichia	235	40	43.5	705	1	DREB_MOUSE	Q9qxs6	mus musculus
163	42	45.7	544	2	Q60B74_METCA	O60b74	methylcoccc	236	40	43.5	706	1	DREB_RAT	Q97266	rattus norv
164	42	45.7	601	1	EPG_DESVH	Q72ci3	desulfovibr	237	40	43.5	745	2	Q8QHJ6_BRARE	Q8qhj6	brachydanio
165	42	45.7	695	2	Q4T969_TETNG	Q4t969	tetraodon n	238	40	43.5	745	2	Q8QHJ9_BRARE	Q8qhj9	brachydanio
166	42	45.7	757	2	Q8W5V7_9CAUD	Q8w5v7	bacteriopho	239	40	43.5	769	2	Q8IMN9_DROME	O8imn9	drosophila
167	42	45.7	819	2	Q4JUT8_GIBZE	Q4j1t8	gibberella	240	40	43.5	788	2	Q8SYG1_DROME	O8syg1	drosophila
168	42	45.7	1106	2	Q8A340_BACTN	O8a340	bacteroides	241	40	43.5	788	2	Q9W4N2_DROME	Q9wn42	drosophila
169	42	45.7	2178	2	Q8I643_PLAF7	O8i643	plasmodium	242	40	43.5	857	1	AKAP1_MOUSE	O8akp1	mouse
170	42	45.7	2553	2	Q6PUE8_PLAFA	O6pue8	plasmodium	243	40	43.5	857	2	Q5SXZ4_MOUSE	O5sxz4	mus musculus
171	41.5	45.1	224	2	Q4PUE9_9BURK	Q4pue9	burkholderi	244	40	43.5	868	2	Q4RJV8_TETNG	Q4rjv8	tetraodon n
172	41	44.6	65	2	Q5BRW2_SCHJA	O5brw2	schistosoma	245	40	43.5	1001	2	Q9YX12_DROME	Q9yx12	drosophila
173	41	44.6	98	1	ANTE_BACSU	O7wy62	bacillus su	246	40	43.5	1010	2	Q7KUY4_DROME	Q7kuy4	drosophila
174	41	44.6	119	2	Q6ZL23_ORYSA	O6zl23	oryza sativ	247	40	43.5	1209	2	Q4WNF8_ASPFU	O4wnf8	aspergillus
175	41	44.6	148	2	Q65941_ECOLI	O65941	escherichia	248	40	43.5	1287	2	Q7YU59_DROME	Q7yu59	drosophila
176	41	44.6	159	2	Q4S878_TETNG	O4s878	tetraodon n	249	40	43.5	1287	2	Q9U5W1_DROME	O9u5w1	drosophila
177	41	44.6	166	2	Q65265_ASF	O65265	african swi	250	40	43.5	1287	2	Q9VL24_DROME	Q9vl24	drosophila

251	251	40	43.5	2703	2	Q9K0T0_NEIMB	Q9k0t0 neiseseria m	324	39	42.4	431	2	Q4QAU4_LEIMA	Q4qau4 leishmania
252	252	40	43.5	3954	2	Q6LEV2_PLASF7	Q6lev2 plasmodium	325	39	42.4	439	2	Q4NVJ0_9DELT	Q4nvj0 anaeromyxob
253	253	40	43.5	4859	2	Q95201_MUSAVI	Q95201 mustela vis	326	39	42.4	444	2	Q21966_CABEL	Q21966 caenorhabdi
254	254	40	43.5	4859	2	Q7M2T9_9CARN	Q7m2t9 mustela sp.	327	39	42.4	446	2	Q61UL2_CABER	Q61ul2 caenorhabdi
255	255	40	43.5	4869	2	Q90985_CHICK	Q90985 gallus gall	328	39	42.4	453	2	Q8XJA0_CLOPE	Q8xja0 clostridium
256	256	40	43.5	4870	1	RYR3_HUMAN	Q15413 homo sapien	329	39	42.4	454	2	Q52GR6_MAGGR	Q52gr6 magnaporthe
257	257	40	43.5	4872	2	Q9TS33_RABIT	Q9ts33 oryctolagus	330	39	42.4	505	1	BUCC_APLCA	P20481 a buccalin
258	258	39.5	42.9	159	2	Q7WVQ0_9PROC	Q7wvq0 uncultured	331	39	42.4	535	2	Q71LX7_LYCES	Q71lx7 lycopersico
259	259	39.5	42.9	159	2	Q7WVP9_9PROC	Q7wvp9 uncultured	332	39	42.4	557	2	Q66842_9UROC	Q66842 oikopleura
260	260	39.5	42.9	159	2	Q7WVP5_9PROC	Q7wvp5 uncultured	333	39	42.4	558	2	Q83NM3_TROW8	Q83nm3 tropheryma
261	261	39.5	42.9	159	2	Q7WVP4_9PROC	Q7wvp4 uncultured	334	39	42.4	589	2	Q7TX53_MYCBO	Q7tx53 mycobacteri
262	262	39.5	42.9	159	2	Q7WVN7_9PROC	Q7wvn7 uncultured	335	39	42.4	590	2	Q6MX04_MYCTU	Q6mx04 mycobacteri
263	263	39.5	42.9	159	2	Q7WVN5_9PROC	Q7wvn5 uncultured	336	39	42.4	600	2	Q83G97_TROWT	Q83g97 tropheryma
264	264	39.5	42.9	159	2	Q7WVN2_9PROC	Q7wvn2 uncultured	337	39	42.4	603	2	Q8VU66_MYCTU	Q8vu66 mycobacteri
265	265	39.5	42.9	159	2	Q7WVL9_9PROC	Q7wvl9 uncultured	338	39	42.4	628	2	Q5BSC3_EMENI	Q5bsc3 aspergillus
266	266	39.5	42.9	159	2	Q7WVL3_9PROC	Q7wvl3 uncultured	339	39	42.4	691	1	EFQ_WOLPM	Q731x7 wolbachia p
267	267	39.5	42.9	159	2	Q7WVK9_9PROC	Q7wvk9 uncultured	340	39	42.4	691	2	Q4W5Y1_DESVU	Q4w5y1 desulfovibr
268	268	39.5	42.9	159	2	Q7WRK9_9PROC	Q7wrk9 uncultured	341	39	42.4	710	2	Q9PYM6_GVXN	Q9pyw6 xestia c-ni
269	269	39.5	42.9	159	2	Q7WS38_9PROC	Q7ws38 uncultured	342	39	42.4	715	2	Q93VM2_ORYSA	Q93vm2 oryza sativ
270	270	39.5	42.9	159	2	Q7WRH5_9PROC	Q7wrh5 uncultured	343	39	42.4	747	2	Q92YQ3_RHIME	Q92yq3 rhizobium m
271	271	39.5	42.9	276	2	Q8THK2_METAC	Q8thk2 methanosarc	344	39	42.4	750	2	Q5AU92_EMENI	Q5au92 schizosacch
272	272	39.5	42.9	363	2	Q8TNX1_METAC	Q8tnx1 methanosarc	345	39	42.4	813	1	EFQ2_SCHPO	Q94429 schizosacch
273	273	39.5	42.9	647	2	Q9PT10_ONCMY	Q9pt10 oncorhynch	346	39	42.4	853	2	Q6OD13_SOLDE	Q6od13 solanum dem
274	274	39.5	42.9	711	2	Q7X668_ORYSA	Q7x668 oryza sativ	347	39	42.4	920	2	Q9GRN4_LEIMA	Q9grn4 leishmania
275	275	39.5	42.9	711	2	Q7XPX3_ORYSA	Q7xpx3 oryza sativ	348	39	42.4	957	2	Q41PQ8_GIBZE	Q41pq8 gibberella
276	276	39.5	42.9	1564	2	Q6DFB8_XENLA	Q6dfb8 xenopus lae	349	39	42.4	1175	2	Q13632_HUMAN	Q13632 homo sapien
277	277	39.5	42.9	1577	1	HLXA_PROMI	P16466 proteus mir	350	39	42.4	1219	2	Q8W555_HUMAN	Q8w555 homo sapien
278	278	39	42.4	63	2	Q74NR9_BACC1	Q13044 scyllorhinu	351	39	42.4	1260	1	ALS1_CANAL	P45910 candida alb
279	279	39	42.4	69	2	Q13044_SCYCA	Q13044 scyllorhinu	352	39	42.4	1260	2	Q5A8L0_CANAL	Q5a8l0 candida alb
280	280	39	42.4	86	2	Q7USB5_SYNPX	Q7usb5 synecococc	353	39	42.4	1260	2	Q5A8T4_CANAL	Q5a8t4 candida alb
281	281	39	42.4	107	2	Q58937_PYRHO	Q58937 pyrococcus	354	39	42.4	1279	2	Q6L3L8_SOLDE	Q6l3l8 solanum dem
282	282	39	42.4	114	2	Q9UP43_HUMAN	Q9up43 homo sapien	355	39	42.4	1359	2	Q8TB57_HUMAN	Q8tb57 homo sapien
283	283	39	42.4	125	2	Q524B3_MAGGR	Q524b3 magnaporthe	356	39	42.4	1372	2	Q87JN6_VIBPA	Q87jnj6 vibrio para
284	284	39	42.4	126	2	Q613E0_CABER	Q613e0 caenorhabdi	357	39	42.4	1373	2	Q8IWE9_HUMAN	Q8iwe9 homo sapien
285	285	39	42.4	126	2	Q19685_CAREL	Q19685 caenorhabdi	358	39	42.4	1385	2	Q9Y4B4_HUMAN	Q9y4b4 homo sapien
286	286	39	42.4	130	2	Q520J2_MAGGR	Q520j2 magnaporthe	359	39	42.4	1427	2	Q14207_HUMAN	Q14207 homo sapien
287	287	39	42.4	171	2	Q4WAT4_ASFFU	Q4wat4 aspergillus	360	39	42.4	1427	2	Q16580_HUMAN	Q16580 homo sapien
288	288	39	42.4	208	2	Q89KL6_BRAJA	Q89kl6 bradyrhizob	361	39	42.4	1466	2	Q99NG0_MOUSE	Q99ng0 mus musculu
289	289	39	42.4	229	2	Q6AQ24_DESPS	Q6aq24 desulfotale	362	39	42.4	1515	2	Q4SXJ6_TETNG	Q4sxxj6 tetraodon n
290	290	39	42.4	233	2	Q9XG55_LORTJA	Q9xg55 lotus japon	363	39	42.4	2029	2	Q41FP4_GIBZE	Q41fp4 gibberella
291	291	39	42.4	240	2	P89268_GVXN	P89268 xestia c-ni	364	39	42.4	3206	2	Q7WK28_BORBR	Q7wk28 bordetella
292	292	39	42.4	245	2	Q8B966_9ROOV	Q8b966 avian ortho	365	39	42.4	3590	1	FXAB_BORPE	P12255 bordetella
293	293	39	42.4	261	2	Q8L316_AZOVI	Q8l316 azotobacter	366	39	42.4	3590	2	Q8VV99_BORPE	Q8vv99 bordetella
294	294	39	42.4	261	2	Q41XW7_AZOVI	Q41xw7 azotobacter	367	39	42.4	3590	2	Q45365_BORPE	Q45365 bordetella
295	295	39	42.4	262	2	Q6YIR5_NECWA	Q6yir5 neurturfs ma	368	39	42.4	3592	2	Q7W692_BORPA	Q7w692 bordetella
296	296	39	42.4	267	2	Q8UBT9_AGR75	Q8ubt9 agrobacteri	369	39	42.4	3634	2	Q9JP78_BORBR	Q9jp78 bordetella
297	297	39	42.4	274	2	Q8W0E7_ORYSA	Q8w0e7 oryza sativ	370	39	42.4	3652	2	Q7W161_BORBR	Q7w161 bordetella
298	298	39	42.4	300	2	Q9K0T3_NEIMB	Q9k0t3 neiseseria m	371	39	42.4	4196	2	Q7VV06_BORPE	Q7vv06 bordetella
299	299	39	42.4	312	2	Q717Q6_9ROOV	Q7t7q6 avian ortho	372	39	42.4	4218	2	Q7W7M5_BORPA	Q7w7m5 bordetella
300	300	39	42.4	314	2	Q899J6_CLOTE	Q899j6 clostridium	373	39	42.4	4218	2	Q7WL14_BORBR	Q7wl14 bordetella
301	301	39	42.4	317	2	Q911E4_9ROOV	Q911e4 lymanthia d	374	38.5	41.8	145	2	Q8ET10_MOUSE	Q8et10 mus musculu
302	302	39	42.4	318	2	Q4U5R9_9ROOV	Q4u5r9 heliothis a	375	38.5	41.8	159	2	Q7WVL2_9PROC	Q7wvl2 uncultured
303	303	39	42.4	326	1	SIGC_ARVSL	Q99212 avian feovi	376	38.5	41.8	218	2	Q8R2V6_MOUSE	Q8r2v6 mus musculu
304	304	39	42.4	326	2	Q12287_9ROOV	Q12287 avian ortho	377	38.5	41.8	261	2	Q6YXSL_ORYSA	Q6yxsl oryza sativ
305	305	39	42.4	326	2	Q8QV12_9ROOV	Q8qv12 avian feovi	378	38.5	41.8	555	1	C78AB_ORYSA	Q7y1v5 oryza sativ
306	306	39	42.4	326	2	Q8QV13_9ROOV	Q8qv13 avian feovi	379	38.5	41.8	783	2	Q53LJ8_ORYSA	Q53lj8 oryza sativ
307	307	39	42.4	326	2	Q8QV17_9ROOV	Q8qv17 avian feovi	380	38.5	41.8	974	2	Q68F88_MOUSE	Q68f88 mus musculu
308	308	39	42.4	326	2	Q9DPB1_9ROOV	Q9dpb1 avian ortho	381	38.5	41.8	1035	2	Q5NTZ0_BOMMO	Q5ntz0 bombyx mori
309	309	39	42.4	326	2	Q9DPB5_9ROOV	Q9dpb5 avian ortho	382	38.5	41.8	1051	2	Q7M4J4_BOMMO	Q7m4j4 bombyx mori
310	310	39	42.4	326	2	Q91CG7_9ROOV	Q91cg7 avian ortho	383	38.5	41.8	1231	2	Q82276_ARATH	Q82276 arabidopsis
311	311	39	42.4	326	2	Q91LM3_9ROOV	Q91lm3 avian ortho	384	38.5	41.8	1657	2	Q4QHB6_LEIMA	Q4qhe6 leishmania
312	312	39	42.4	326	2	Q91LM4_9ROOV	Q91lm4 avian ortho	385	38.5	41.8	2310	1	ABCA4_MOUSE	Q35600 mus musculu
313	313	39	42.4	326	2	Q91LM5_9ROOV	Q91lm5 avian ortho	386	38	41.3	100	2	Q8CEL8_MOUSE	Q8cel8 mus musculu
314	314	39	42.4	326	2	Q91LB6_9ROOV	Q91lb6 avian feovi	387	38	41.3	100	2	Q4SPB9_TETNG	Q4spb9 tetraodon n
315	315	39	42.4	326	2	Q51238_ARVSL	Q5i238 avian reovi	388	38	41.3	119	2	Q5AHC5_CANAL	Q5ahc5 candida alb
316	316	39	42.4	326	2	Q4U515_9ROOV	Q4u515 avian ortho	389	38	41.3	130	2	Q9T040_ARATH	Q9t040 arabidopsis
317	317	39	42.4	327	2	Q66637_9GAMA	Q66637 equid herpe	390	38	41.3	134	2	Q5Q0B1_ARATH	Q5q0b1 arabidopsis
318	318	39	42.4	331	2	Q8W0E7_CABEL	Q8w0e7 caenorhabdi	391	38	41.3	142	2	Q13032_BRACHD	Q13032 brachidanio
319	319	39	42.4	338	2	Q9C8D5_ARATH	Q9c8d5 arabidopsis	392	38	41.3	147	2	Q9EUM5_CORGL	Q9eum5 corynebacte
320	320	39	42.4	369	2	Q8SUP9_ENCCU	Q8sup9 encephalito	393	38	41.3	149	2	Q9LCV3_PARDE	Q9lcv3 paracoccus
321	321	39	42.4	413	2	Q8BGB4_MOUSE	Q8bgb4 m mus muscu	394	38	41.3	168	2	Q69RM9_ORYSA	Q69rm9 oryza sativ
322	322	39	42.4	423	2	Q4WYR5_ASPPFU	Q4wyr5 aspergillus	395	38	41.3	184	2	Q6W1B9_RHISN	Q6w1b9 rhizobium s
323	323	39	42.4	426	2	Q88QW2_PSEPK	Q88qw2 pseudomonas	396	38	41.3	193	2	Q8BPPY2_MOUSE	Q8bpy2 mus musculu

397	38	41.3	215	2	Q5NQU9_ZYMMO	Q5nqu9 zymomonas m	470	38	41.3	777	2	Q8IMM1_DROME	Q8imm1 drosophila
398	38	41.3	216	2	Q5INW8_MAGGR	Q5inw8 magnaporthe	471	38	41.3	785	2	Q5V1X1_HALMA	Q5v1x1 haloarcula
399	38	41.3	230	2	Q6BP30_ORYSA	Q6bp30 oryza sativ	472	38	41.3	803	1	UBP14_YEAST	UBp14 yeast
400	38	41.3	239	2	Q75GDO_ORYSA	Q75gd0 oryza sativ	473	38	41.3	808	2	Q3VAU1_DROME	Q3vau1 drosophila
401	38	41.3	244	2	Q8X0R4_NEUCR	Q8x0r4 neurospora	474	38	41.3	809	2	Q5T232_HUMAN	Q5t232 homo sapien
402	38	41.3	246	1	PSTB_CAMJE	Q9phq1 campylobact	475	38	41.3	819	1	EFG2_YEAST	EFg2 yeast
403	38	41.3	246	2	Q4HHU4_CAMCO	Q4hhu4 campylobact	476	38	41.3	819	2	Q8TEE5_HUMAN	Q8tee5 saccharomyc
404	38	41.3	246	2	Q4HKD6_CAMLA	Q4hk46 campylobact	477	38	41.3	893	2	Q8U9E1_AGR5	Q8uee1 agrobacteri
405	38	41.3	246	2	Q5HV44_CAMJR	Q5hvf4 campylobact	478	38	41.3	900	2	Q7CTB1_AGR5	Q7ctb1 agrobacteri
406	38	41.3	247	2	Q9NXZ6_HUMAN	Q9nxz6 homo sapien	479	38	41.3	922	2	Q678D6_VIRU	Q678d6 lymphocysti
407	38	41.3	248	2	Q8A260_BACTN	Q8a260 bacteroides	480	38	41.3	1045	2	Q9LET7_ARATH	Q9let7 arabidopsis
408	38	41.3	248	2	Q9BMG3_AMEPV	Q9emg3 amoeba moo	481	38	41.3	1039	2	Q7SCH0_NEUCR	Q7sch0 neurospora
409	38	41.3	254	2	Q6ZS66_HUMAN	Q6zsg6 amoeba moo	482	38	41.3	1039	2	Q8X014_NEUCR	Q8x014 neurospora
410	38	41.3	257	2	Q7ZP25_SPHEL	Q7z2p5 spingomonas	483	38	41.3	1046	2	Q6CWM7_KLULA	Q6cwm7 kluyveromyc
411	38	41.3	257	2	Q4S4A8_TETNG	Q4s4a8 tetraodon n	484	38	41.3	1067	2	Q01419_BOMMO	Q01419 bombyx mori
412	38	41.3	260	2	Q7S793_NEUCR	Q7s793 neurospora	485	38	41.3	1097	2	Q4IFMG_GIBZE	Q4ifm8 gibberella
413	38	41.3	269	2	Q8S135_RHOSH	Q8s135 rhodobacter	486	38	41.3	1124	1	PHYA1_TOBAC	PHYA9330 nicotiana t
414	38	41.3	280	1	SOX21_CHICK	Q9w7r5 gallus gall	487	38	41.3	1125	1	PHYA1_POPTM	PHYA9934 populus tre
415	38	41.3	283	2	Q5YWR3_NOCFA	Q5ywr3 nocardia fa	488	38	41.3	1219	2	Q4RXI5_TETNG	Q4rx15 tetraodon n
416	38	41.3	295	2	Q5TNI1_ANOGA	Q5tni1 anopheles g	489	38	41.3	1223	2	Q5ZAP0_ORYSA	Q5zap0 oryza sativ
417	38	41.3	296	2	Q6H6J4_ORYSA	Q6h6j4 oryza sativ	490	38	41.3	1230	2	Q4UD90_THEAN	Q4ud90 theileria a
418	38	41.3	297	2	Q5IRL9_MAGGR	Q5irl9 magnaporthe	491	38	41.3	1320	2	Q4SMW6_TETNG	Q4smw6 tetraodon n
419	38	41.3	297	2	Q5N8V8_ORYSA	Q5n8v8 oryza sativ	492	38	41.3	1730	2	Q516W5_ENTHI	Q516w5 entamoeba h
420	38	41.3	299	2	Q8NU39_ENCCU	Q8nu39 encephalito	493	38	41.3	2151	2	Q8H898_ORYSA	Q8h898 oryza sativ
421	38	41.3	319	2	Q724D8_LISMP	Q724d8 listeria mo	494	38	41.3	2261	2	Q5HCP3_STAAC	Q5hcp3 staphylococ
422	38	41.3	319	2	Q8YA92_LISMO	Q8ya92 listeria mo	495	37.5	40.8	121	2	Q77653_MACMU	Q77653 macaca mula
423	38	41.3	319	2	Q92F16_LISIN	Q92f16 listeria in	496	37.5	40.8	159	2	Q7WVN3_PROUC	Q7wvn3 uncultured
424	38	41.3	347	2	Q9HLZ4_THEAC	Q9hlz4 thermoplasma	497	37.5	40.8	265	2	Q6LXN3_TETMP	Q6lxn3 methanococ
425	38	41.3	347	2	Q92X29_RHIME	Q92x29 rhizobium m	498	37.5	40.8	289	2	Q4ZXI5_PSEES	Q4zx15 pseudomonas
426	38	41.3	353	2	Q8LA09_ARATH	Q8la09 arabidopsis	499	37.5	40.8	289	2	Q886Y2_PSESM	Q886y2 pseudomonas
427	38	41.3	353	2	Q9LFC7_ARATH	Q9lfc7 arabidopsis	500	37.5	40.8	302	2	Q5FQJ6_GLUOX	Q5fqj6 gluconobact
428	38	41.3	356	1	PCBP1_HUMAN	Q15365 homo sapien	501	37.5	40.8	303	2	Q9PML2_PETMO	Q9pml2 petromyzon
429	38	41.3	356	1	PCBP1_MOUSE	P60335 mus musculus	502	37.5	40.8	563	2	Q57Y26_9TRYP	Q57y26 trypanosoma
430	38	41.3	356	1	PCBP1_RABIT	Q19048 oryctolagus	503	37.5	40.8	650	2	Q6LDL6_CABER	Q6ldl6 caenorhabdi
431	38	41.3	356	1	Q53S88_HUMAN	Q53s88 homo sapien	504	37.5	40.8	687	2	Q9FJ32_ARATH	Q9fj32 arabidopsis
432	38	41.3	356	2	Q5E9A3_BOVIN	Q5e9a3 bos taurus	505	37.5	40.8	707	2	Q4RJ44_TETNG	Q4rjr4 tetraodon n
433	38	41.3	362	1	CBX8_MOUSE	Q9qrv1 mus musculus	506	37.5	40.8	728	2	Q6AT76_ORYSA	Q6at76 oryza sativ
434	38	41.3	369	1	VP6_AHSV6	Q64913 african hor	507	37.5	40.8	904	2	Q5WMQ4_ORYSA	Q5wmq4 oryza sativ
435	38	41.3	399	2	Q4LH94_9BURK	Q4lh94 burkholderi	508	37.5	40.8	904	2	Q59666_SCHPO	Q59666 schizosacch
436	38	41.3	405	2	Q6K235_ORYSA	Q6k235 oryza sativ	509	37.5	40.8	1015	2	Q6D7B7_ERWCT	Q6d7b7 erwinia car
437	38	41.3	414	2	Q4WTA4_ASPFU	Q4wt44 aspergillus	510	37.5	40.8	2142	2	Q5FWR3_ARATH	Q5fwr3 arabidopsis
438	38	41.3	427	2	Q98L45_RHILLO	Q98l45 rhizobium l	511	37.5	40.8	4864	2	Q5RQ04_BRARE	Q5rq04 brachydanio
439	38	41.3	439	2	Q5B3L4_EMENI	Q5b3l4 aspergillus	512	37	40.2	30	2	Q53WY7_HUMAN	Q53wy7 homo sapien
440	38	41.3	471	2	Q4T608_TETNG	Q4t608 tetraodon n	513	37	40.2	57	2	Q8XHU1_CLOPE	Q8xhu1 clostridium
441	38	41.3	517	1	FOXNA_HUMAN	Q96nz1 homo sapien	514	37	40.2	68	2	Q8YIC8_RALSO	Q8ylc8 ralstonia s
442	38	41.3	517	2	Q9VL04_DROME	Q9vl04 drosophila	515	37	40.2	77	2	Q95J81_HORSE	Q95j81 equus cabal
443	38	41.3	521	2	Q4Q977_LEIMA	Q4q977 leishmania	516	37	40.2	96	2	Q5ZUE2_LEGPH	Q5zue2 legionella
444	38	41.3	524	2	Q8S220_ORYSA	Q8s220 oryza sativ	517	37	40.2	96	2	Q5ZUE2_LEGPH	Q5zue2 corynebacte
445	38	41.3	542	2	Q755A6_ASHGO	Q755a6 ashbya goss	518	37	40.2	100	2	Q69L15_ORYSA	Q69l15 oryza sativ
446	38	41.3	544	2	Q4NBS7_5MICC	Q4nbs7 arthroabacte	519	37	40.2	110	2	Q4XV2_CORJK	Q4xv2 corynebacte
447	38	41.3	550	2	Q8IPC4_DROME	Q8ipc4 drosophila	520	37	40.2	116	2	Q5NMW4_AZOSE	Q5nmw4 azoarcus sp
448	38	41.3	550	2	Q9DGC30_BRARE	Q9dgc30 brachydanio	521	37	40.2	120	2	Q864T8_MONDO	Q864t8 monodelphis
449	38	41.3	550	2	Q9PT94_BRARE	Q9pt94 brachydanio	522	37	40.2	123	2	Q7YWC9_TENMO	Q7ywc9 tenobrio mo
450	38	41.3	551	2	Q8IPC3_DROME	Q8ipc3 drosophila	523	37	40.2	131	2	Q4I710_GIBZE	Q4i710 gibberella
451	38	41.3	555	2	Q4UFI6_THEAN	Q4ufj6 theileria a	524	37	40.2	133	2	Q69775_RHJET	Q69775 rhizobium e
452	38	41.3	556	2	Q9C2M0_NEUCR	Q9c2m0 neurospora	525	37	40.2	137	2	Q69775_RHJET	Q69775 rhizobium e
453	38	41.3	557	2	Q7Q553_ANOGR	Q7q553 anopheles g	526	37	40.2	138	2	Q9YF84_AERPE	Q9yf84 aeropyrum p
454	38	41.3	559	2	Q9AP81_9PSED	Q9ap81 pseudomonas	527	37	40.2	145	2	Q87GP8_VIBPA	Q87gp8 vibrio para
455	38	41.3	563	1	HNMI_YEAST	P19807 saccharomyc	528	37	40.2	146	2	Q6L3Z1_SOIDE	Q6l3z1 solanum dem
456	38	41.3	571	2	Q5JWA3_ORYSA	Q5jwa3 oryza sativ	529	37	40.2	149	2	Q5EP97_NEIGO	Q5ep97 neisseria g
457	38	41.3	579	2	Q6ISU3_ORYSA	Q6isu3 oryza sativ	530	37	40.2	151	2	Q6BL90_DEBHA	Q6bl90 debaryomyce
458	38	41.3	591	2	Q753P7_ASHGO	Q753p7 ashbya goss	531	37	40.2	153	2	Q52AB7_MAGGR	Q52ab7 magnaporthe
459	38	41.3	597	2	Q4I8N7_GIBZE	Q4i8n7 gibberella	532	37	40.2	155	2	Q755Z1_ASHGO	Q755z1 ashbya goss
460	38	41.3	613	2	Q4QDB7_LEIMA	Q4qdb7 leishmania	533	37	40.2	155	2	Q9RIG1_RAT	Q9rig1 rattus norv
461	38	41.3	639	2	Q8IPC5_DROME	Q8ipc5 drosophila	534	37	40.2	157	2	Q53M19_ORYSA	Q53m19 oryza sativ
462	38	41.3	639	2	Q8SVF0_DROME	Q8svf0 drosophila	535	37	40.2	161	2	Q6LCX4_PIG	Q6lcx4 sus scrofa
463	38	41.3	683	1	EPG1_TREDE	Q73r08 treponema d	536	37	40.2	162	2	Q7PX88_ANOGA	Q7px88 anopheles g
464	38	41.3	683	1	EPG2_TREPA	Q83464 treponema p	537	37	40.2	164	2	Q9PEF9_XYLFA	Q9pef9 xyloella fas
465	38	41.3	690	1	EPG2_TREPA	Q5pbh2 anaplasmam	538	37	40.2	168	2	Q9D382_MOUSE	Q9d382 mus musculus
466	38	41.3	720	2	Q8PSM7_METWA	Q8psm7 methanosarc	539	37	40.2	175	2	Q6ZVA0_HUMAN	Q6zva0 homo sapien
467	38	41.3	725	2	Q4IRU0_GIBZE	Q4iru0 gibberella	540	37	40.2	186	2	Q8HB22_9PRIM	Q8hb22 gorilla gor
468	38	41.3	735	2	Q9W3N8_DROME	Q9w3n8 drosophila	541	37	40.2	187	1	EM11_YEAST	EM11 yeast
469	38	41.3	740	2	Q96MT1_HUMAN	Q96mt1 homo sapien	542	37	40.2	191	2	Q5PEM4_XENTR	Q5pem4 xenopus tro

543	37	40.2	202	2	Q9ETD1_STRCO	Q9etd1 streptomyce	616	37	40.2	403	2	Q4SPX0_TETNG	Q4spx0 tetraodon n
544	37	40.2	207	2	Q4UQU0_XANCP	Q4uqu0 xanthomonas	617	37	40.2	408	2	Q9D3Y6_MOUSE	Q9d3y6 mus musculus
545	37	40.2	207	2	Q8PCN0_XANCP	Q8pcn0 xanthomonas	618	37	40.2	413	2	Q4R3R4_MACFA	Q4r3r4 macaca fasc
546	37	40.2	207	2	Q8PPD9_XANAC	Q8ppd9 xanthomonas	619	37	40.2	416	2	Q86913_9SPHN	Q86913 spingomona
547	37	40.2	213	2	Q9LNE1_ARATH	Q9lne1 arabidopsis	620	37	40.2	421	2	Q8GT90_PRUPE	Q8gt90 prunus pers
548	37	40.2	215	2	Q99QK8_STRCO	Q99qk8 streptomyce	621	37	40.2	427	2	Q6XQD8_9CAUD	Q6xqd8 enterobacte
549	37	40.2	218	2	Q7YT12_RHOPR	Q7yt12 rhodnius pr	622	37	40.2	431	2	Q5ZJP3_CHICK	Q5zjp3 gallus gall
550	37	40.2	235	2	Q9UZ11_CABEL	Q9uz11 caenorhabdi	623	37	40.2	434	2	Q56XT1_ARATH	Q56xt1 arabidopsis
551	37	40.2	238	1	MINC_CANBF	Q7vqz1 candidatus	624	37	40.2	442	2	Q758Q5_ASHGO	Q758q5 ashbya goss
552	37	40.2	239	2	Q6UC92_MELGA	Q6uc92 melagris g	625	37	40.2	450	2	Q7UUP7_RHOBG	Q7uup7 rhodopirell
553	37	40.2	241	2	Q8EJR6_SHEON	Q8ejr6 shewanella	626	37	40.2	465	2	Q6H3Z1_ORYSA	Q6h3z1 oryza sativ
554	37	40.2	247	1	TR140_RAT	Q8mfy8 rattus norv	627	37	40.2	467	2	Q6K5K9_ORYSA	Q6k5k9 oryza sativ
555	37	40.2	248	2	Q4I266_GIBZE	Q4i266 gibberella	628	37	40.2	468	1	STE11_SCHPO	P36631 schizosacch
556	37	40.2	254	2	Q5NTN0_9BACT	Q5ntn0 uncultured	629	37	40.2	486	2	Q7R4M1_GIALA	Q7r4m1 giardia lam
557	37	40.2	257	1	CR010_HUMAN	Q68c15 homo sapien	630	37	40.2	491	2	Q5CYK6_CRYPV	Q5cyk6 cryptospori
558	37	40.2	257	2	Q6VAX1_ANOGA	Q6vax1 anopheles g	631	37	40.2	495	2	Q59HF0_HUMAN	Q59hf0 homo sapien
559	37	40.2	257	2	Q6VAX3_ANOGA	Q6vax3 anopheles g	632	37	40.2	496	2	Q6RXW9_9DIPT	Q6rxw9 anopheles p
560	37	40.2	257	2	Q6VAX4_ANOGA	Q6vax4 anopheles g	633	37	40.2	496	2	Q4NRN3_9DELT	Q4nrn3 anaeronyxob
561	37	40.2	260	1	BMBE1_HUMAN	Q13145 homo sapien	634	37	40.2	502	2	Q5Z3P3_MAGGR	Q5z3p3 magnaporthe
562	37	40.2	260	2	Q53G66_HUMAN	Q53g66 homo sapien	635	37	40.2	502	2	Q4S499_TETNG	Q4s499 tetraodon n
563	37	40.2	260	2	Q8UD87_AGR75	Q8ud87 agrobacteri	636	37	40.2	505	2	Q5F6J9_NEIG1	Q5f6j9 neisseria g
564	37	40.2	262	2	Q9WH90_HHV8	Q9wh90 human herpe	637	37	40.2	508	2	Q7DDQ5_NEIMB	Q7ddq5 neisseria m
565	37	40.2	267	1	COLI_HUMAN	P01189 h corticotr	638	37	40.2	508	2	Q9JR87_NEIMA	Q9jr87 neisseria m
566	37	40.2	267	2	Q5TZZ7_HUMAN	Q5tzz7 homo sapien	639	37	40.2	511	2	Q5AS84_EMENI	Q5as84 aspergillus
567	37	40.2	267	2	Q6FHC8_HUMAN	Q6fnc8 homo sapien	640	37	40.2	512	2	Q8MRJ5_DROME	Q8mrj5 drosophila
568	37	40.2	267	2	Q53T23_HUMAN	Q53t23 homo sapien	641	37	40.2	512	2	Q8BGV4_MOUSE	Q8bgv4 m mus muscu
569	37	40.2	269	2	Q7XVH5_ORYSA	Q7xvh5 oryza sativ	642	37	40.2	512	2	Q8VE31_MOUSE	Q8ve31 mus musculus
570	37	40.2	274	2	Q4J109_AZOFI	Q4j109 azotobacter	643	37	40.2	513	2	Q4MY42_BACCE	Q4my42 bacillus ce
571	37	40.2	275	2	Q6AQ9S_DESPS	Q6aq9s desulfotale	644	37	40.2	513	2	Q6HFU3_BACHK	Q6hfu3 bacillus th
572	37	40.2	275	2	Q7M9A2_WOLSU	Q7m9a2 wolinnella s	645	37	40.2	513	2	Q8IYJ4_BACCR	Q8iyj4 bacillus ce
573	37	40.2	279	2	Q7IME9_DICLA	Q7ime9 dicentrarch	646	37	40.2	513	2	Q8IYJ4_BACAN	Q8iyj4 bacillus an
574	37	40.2	281	2	Q4HNN1_CAMCO	Q4hnn1 campylobact	647	37	40.2	514	2	Q4VXB1_MOUSE	Q4vbx1 mus musculus
575	37	40.2	281	2	Q4HKB9_CAMLA	Q4hbk9 campylobact	648	37	40.2	528	2	Q6J4K1_HUMAN	Q6j4k1 gibberella
576	37	40.2	281	2	Q4HRK1_CAMUP	Q4hrk1 campylobact	649	37	40.2	528	2	Q6J4K1_HUMAN	Q6j4k1 homo sapien
577	37	40.2	281	2	Q5PHX7_CAMJE	Q5phx7 campylobact	650	37	40.2	531	2	Q6INH9_XENLA	Q6inh9 xenopus lae
578	37	40.2	281	2	Q5HVM9_CAMJR	Q5hvm9 campylobact	651	37	40.2	533	2	Q9AQ54_BACME	Q9aq54 bacillus me
579	37	40.2	282	2	Q6MDV8_PARUW	Q6mdv8 parachlamyid	652	37	40.2	537	2	Q8BNA7_MOUSE	Q8bna7 mus musculus
580	37	40.2	284	2	Q8MLV8_DROME	Q8mlv8 drosophila	653	37	40.2	543	2	Q949X8_ARATH	Q949x8 arabidopsis
581	37	40.2	285	2	Q4ZR22_PSESY	Q4zr22 pseudomonas	654	37	40.2	551	2	Q55347_9VIRU	Q55347 bermajo vir
582	37	40.2	286	1	KORB_METTH	Q27113 methanobact	655	37	40.2	564	2	Q5CTZ7_CRYPV	Q5ctz7 cryptospori
583	37	40.2	287	2	Q9VJ98_DROME	Q9vj98 drosophila	656	37	40.2	570	2	Q7BJ43_ANOGA	Q7bj43 anopheles g
584	37	40.2	287	2	Q5UL40_DROME	Q5ul40 drosophila	657	37	40.2	575	2	Q9HKB5_THEAC	Q9hkb5 thermoplasma
585	37	40.2	288	2	Q7NKG4_GLOVI	Q7nkg4 gloeobacter	658	37	40.2	579	2	Q5IX68_MAGGR	Q5ix68 magnaporthe
586	37	40.2	292	2	Q5AWT3_EMENI	Q5awt3 aspergillus	659	37	40.2	581	1	LRTM3_HUMAN	Q86vh5 homo sapien
587	37	40.2	299	2	Q4SLP2_TETNG	Q4slp2 tetraodon n	660	37	40.2	581	2	LRTM3_MACFA	Q9bq36 macaca fasc
588	37	40.2	300	2	Q4KN59_HUMAN	Q4kn59 homo sapien	661	37	40.2	582	1	LRTM3_MOUSE	Q8bz81 mus musculus
589	37	40.2	300	2	Q5RBT9_PONPY	Q5rbt9 pongo pygma	662	37	40.2	582	2	Q8EZA0_MOUSE	Q8beza0 mus musculu
590	37	40.2	303	2	Q9PAK5_XILFA	Q9pak5 xyella fas	663	37	40.2	584	2	Q4IA69_GIBZE	Q4ia69 gibberella
591	37	40.2	306	2	Q5GQW4_9CAUD	Q5gqw4 bacterioph	664	37	40.2	584	2	Q6J4K2_HUMAN	Q6j4k2 homo sapien
592	37	40.2	317	2	Q52960_RHIME	Q52960 rhizobium m	665	37	40.2	584	2	Q4KMS9_HUMAN	Q4kms9 homo sapien
593	37	40.2	317	2	Q7UU28_RHOBG	Q7uu28 rhodopirell	666	37	40.2	585	2	Q925Q3_MOUSE	Q925q3 mus musculus
594	37	40.2	317	2	Q7VEM5_MYCBO	Q7vem5 mycobacteri	667	37	40.2	585	2	Q6AXS0_RAT	Q6axs0 rattus norv
595	37	40.2	317	2	Q53537_MYCTU	Q53537 mycobacteri	668	37	40.2	589	2	Q9JUD9_NEIMA	Q9jud9 neisseria m
596	37	40.2	319	2	Q4LQU8_9BURK	Q4lqu8 burkholderi	669	37	40.2	589	2	Q9JS33_NEIMB	Q9js33 neisseria m
597	37	40.2	319	2	Q4MWG8_BACCE	Q4mwg8 bacillus ce	670	37	40.2	591	2	Q4LLQ2_9BURK	Q4llq2 burkholderi
598	37	40.2	319	2	Q816S2_BACCR	Q816s2 bacillus ce	671	37	40.2	591	2	Q4KG06_PBEF5	Q4kg06 pseudomonas
599	37	40.2	319	2	Q72YX8_BACC1	Q72yx8 bacillus ce	672	37	40.2	594	2	Q63UZ2_BURPS	Q63uz2 burkholderi
600	37	40.2	319	2	Q81KJ6_BACAN	Q81kj6 bacillus an	673	37	40.2	594	2	Q92TV7_RHIME	Q92tv7 rhizobium m
601	37	40.2	319	2	Q6HCD3_BACHK	Q6hcd3 bacillus th	674	37	40.2	596	1	HMEN_ANOGA	Q02491 anopheles g
602	37	40.2	319	2	Q63ZU3_BACCC	Q63zu3 bacillus ce	675	37	40.2	596	2	Q89QG2_BRAJA	Q89qg2 bradyrhizob
603	37	40.2	323	2	Q56B05_TREHY	Q56b05 treponema h	676	37	40.2	597	2	Q95LG7_CANFA	Q95lg7 canis famli
604	37	40.2	329	2	Q57Y13_9TRYP	Q57y13 trypanosoma	677	37	40.2	598	2	Q5Z5K6_ORYSA	Q5z5k6 oryza sativ
605	37	40.2	339	2	Q6XB22_ACIBA	Q6xb22 acinetobact	678	37	40.2	598	2	Q6ES92_ORYSA	Q6es92 oryza sativ
606	37	40.2	349	2	Q9XXM4_CABEL	Q9xxm4 caenorhabdi	679	37	40.2	614	2	Q5CKU6_CRYHO	Q5cku6 cryptospori
607	37	40.2	351	2	Q5WNW0_AZOSE	Q5wnw0 azocarc sp	680	37	40.2	620	2	Q5CI25_CRYHO	Q5ci25 cryptospori
608	37	40.2	360	2	Q8MQU3_PARLI	Q8mqu3 paracentrot	681	37	40.2	621	2	Q5KGY3_CRYNE	Q5kg33 cryptococcu
609	37	40.2	361	2	Q9C6M5_ARATH	Q9c6m5 arabidopsis	682	37	40.2	621	2	Q5SSJ4_CRYNE	Q5ssj4 cryptococcu
610	37	40.2	361	2	Q4KKZ3_MOUSE	Q4kkz3 mus musculus	683	37	40.2	624	2	Q94487_SCHPO	Q94487 schizosacch
611	37	40.2	373	2	Q82389_ARATH	Q82389 arabidopsis	684	37	40.2	626	2	Q8N631_HUMAN	Q8n631 homo sapien
612	37	40.2	376	2	Q9RU26_DEIRA	Q9ru26 deinococcus	685	37	40.2	627	1	S13A4_HUMAN	Q9ukg4 homo sapien
613	37	40.2	379	2	Q9SJF9_MOUSE	Q9sjf9 mus musculus	686	37	40.2	641	2	Q82P23_STRAW	Q82p29 streptomyce
614	37	40.2	389	2	Q9H618_HUMAN	Q9h618 homo sapien	687	37	40.2	648	2	Q5VON4_HALMA	Q5von4 haloarcula
615	37	40.2	399	2	Q64QU0_BACFR	Q64qu0 bacteroides	688	37	40.2	679	2	Q5PXH3_CANTR	Q5pxh3 candida tro

689	37	40.2	2	Q66T17 CANTR	Q66t17 candida tro	762	36.5	39.7	68	2	Q8EHA6 SHEON	Q8Eha6 shewanelia
690	37	40.2	2	Q7Q177 ANOGA	Q7q177 anopheles g	763	36.5	39.7	93	2	Q7ZPU7 9HIV1	Q7zpu7 human immun
691	37	40.2	2	Q8BRF4 MOUSE	Q8brf4 mus musculus	764	36.5	39.7	131	2	Q9WV4 9HIV1	Q9wfv4 human immun
692	37	40.2	2	Q5TX14 ANOGA	Q5tx14 anopheles g	765	36.5	39.7	140	1	LYSA DROME	P83971 drosophila
693	37	40.2	701	1 EFG1 BDEBA	Q6mj13 bdellovibri	766	36.5	39.7	140	1	LYSD DROME	P83972 drosophila
694	37	40.2	726	2 Q5XDK4 STRP6	Q5xdk4 streptococc	767	36.5	39.7	148	2	Q6R7B2 9HERP	Q6r7b2 ostreid her
695	37	40.2	726	2 Q8K8G3 STRP6	Q8k8g3 streptococc	768	36.5	39.7	159	2	Q7WVQ6 9PROC	Q7wvq6 uncultured
696	37	40.2	726	2 Q8R295 STRP8	Q8r295 streptococc	769	36.5	39.7	159	2	Q7WVQ5 9PROC	Q7wvq5 uncultured
697	37	40.2	726	2 Q9A175 STRPY	Q9a175 streptococc	770	36.5	39.7	159	2	Q7WVQ4 9PROC	Q7wvq4 uncultured
698	37	40.2	748	2 Q4H3H8 CIOIN	Q4h3h8 ciona intes	771	36.5	39.7	159	2	Q7WVQ3 9PROC	Q7wvq3 uncultured
699	37	40.2	762	2 Q4SIL4 TETNG	Q4sil4 tetraodon n	772	36.5	39.7	159	2	Q7WVN6 9PROC	Q7wvn6 uncultured
700	37	40.2	774	2 Q7SBS3 NEURC	Q7sbs3 neurospora	773	36.5	39.7	159	2	Q7WVN3 9PROC	Q7wvn3 uncultured
701	37	40.2	776	2 Q8O963 ARATH	Q8o963 arabidopsis	774	36.5	39.7	159	2	Q7WVN2 9PROC	Q7wvn2 uncultured
702	37	40.2	781	2 Q7QCM0 ANOGA	Q7qcm0 anopheles g	775	36.5	39.7	159	2	Q7WVW1 9PROC	Q7wvwl1 uncultured
703	37	40.2	783	2 Q94BR7 ARATH	Q94br7 arabidopsis	776	36.5	39.7	159	2	Q7WVW6 9PROC	Q7wvwl6 uncultured
704	37	40.2	788	2 Q9S175 ARATH	Q9s175 arabidopsis	777	36.5	39.7	168	2	Q6YQ78 ONYPE	Q6yq78 onion yello
705	37	40.2	788	1 EFGC SOYBN	P348l1 glycine max	778	36.5	39.7	197	2	Q6ZVZ6 HUMAN	Q6zvz6 homo sapien
706	37	40.2	807	2 Q6FLG2 CANGA	Q6flg2 candida gla	779	36.5	39.7	253	2	Q7WBL3 BORPA	Q7wbl3 bordetella
707	37	40.2	811	1 MUTS_THEAQ	Q56215 thermus aqu	780	36.5	39.7	315	2	Q9F696 BARBA	Q9f696 bartonella
708	37	40.2	811	1 MUTS_THET2	P61671 thermus the	781	36.5	39.7	409	2	Q8GY67 ARATH	Q8gy67 arabidopsis
709	37	40.2	817	1 MUTS_THETCA	Q921x6 thermus cal	782	36.5	39.7	424	2	Q9LR24 ARATH	Q9lr24 arabidopsis
710	37	40.2	818	1 MUTS_THET8	Q56239 thermus the	783	36.5	39.7	466	2	Q98HE2 RHIL0	Q98he2 rhizobium l
711	37	40.2	839	2 Q6O6V3 METCA	Q6o6v3 methylococc	784	36.5	39.7	468	2	Q8AAM8 BACTN	Q8aam8 bacteroides
712	37	40.2	844	2 Q89KQ1 BRAJA	Q89kq1 bradyrhizob	785	36.5	39.7	500	2	Q6H1N9 9HIV1	Q6h1n9 human immun
713	37	40.2	854	1 AKAP1_RAT	Q88884 r a kinase	786	36.5	39.7	534	2	Q4ICL6 GIBZE	Q4icl6 gibberella
714	37	40.2	869	2 Q8C4I8 MOUSE	Q8c4i8 mus musculu	787	36.5	39.7	551	2	Q4NSA3 9DELT	Q4nsa3 anaeromyxob
715	37	40.2	876	2 Q4Q4D8 LEIMA	Q4q4d8 leishmania	788	36.5	39.7	729	2	Q8UD39 AGRT5	Q8ud39 agrobacteri
716	37	40.2	902	2 Q6CEZ5 YARLI	Q6cezs yarrowia li	789	36.5	39.7	822	2	Q53LL1 ORISA	Q53ll1 oryza sativ
717	37	40.2	915	2 Q99ME3 MOUSE	Q99me3 mus musculu	790	36.5	39.7	1014	2	Q6BT63 DEBHA	Q6bt63 debaromyce
718	37	40.2	930	2 Q8IHH1 DROME	Q8ihh1 drosophila	791	36.5	39.7	1510	2	Q8PHK6 XANAC	Q8phk6 xanthomonas
719	37	40.2	931	2 Q9VP92 DROME	Q9vf92 drosophila	792	36.5	39.7	1747	2	Q57U50 9TRYP	Q57u50 trypanosoma
720	37	40.2	936	1 MSHA_HUMAN	Q15457 homo sapien	793	36	39.1	41	2	Q7PD24 GIALA	Q7pd24 giardia lam
721	37	40.2	936	1 RPOP_CIAPU	P22372 claviceps p	794	36	39.1	48	2	Q95ML1 ATEBE	Q95ml1 ateles belz
722	37	40.2	936	2 Q5VVS4 HOM0 SAPIEN	Q5vvs4 homo sapien	795	36	39.1	57	2	Q6WGN5 CVHSA	Q6wgn5 sars corona
723	37	40.2	965	2 Q4KMM4 MOUSE	Q4kmm4 mus musculu	796	36	39.1	62	2	Q7XB64 ORISA	Q7xb64 oryza sativ
724	37	40.2	1005	2 Q7PT05 ANOGA	Q7pt05 anopheles g	797	36	39.1	69	2	Q4KZM1 9HIV1	Q4kzm1 human immun
725	37	40.2	1048	2 Q5SNL4 ORYSA	Q5snl4 oryza sativ	798	36	39.1	100	2	Q4KZM2 9HIV1	Q4kzm2 human immun
726	37	40.2	1075	1 NFAC3_HUMAN	Q12968 homo sapien	799	36	39.1	104	2	Q8CF33 MOUSE	Q8cf33 mus musculu
727	37	40.2	1100	2 Q6CK25 KLJULA	Q6ck25 kluyveromyc	800	36	39.1	107	2	Q12023 YEAST	Q12023 saccharomyc
728	37	40.2	1113	2 Q7PNE2 ANOGA	Q7pne2 anopheles g	801	36	39.1	136	2	Q9Y3V0 HUMAN	Q9y3v0 homo sapien
729	37	40.2	1123	2 Q6V7X2 OROMI	Q6v7x2 orobandhe m	802	36	39.1	139	2	Q5MA01 TOBAC	Q5ma01 nicotiana t
730	37	40.2	1128	2 Q51N14 MAGGR	Q51n14 magnaporth	803	36	39.1	145	2	Q7VIZ3 HBILHP	Q7vizi3 helicobacte
731	37	40.2	1128	2 P79271_PIG	P79271 sus scrofa	804	36	39.1	147	1	Q6OSC1 CAEBR	Q6osc1 caenorhabdi
732	37	40.2	1190	2 Q68SS4 9AGAR	Q68ss4 pleurotus s	805	36	39.1	147	1	REV_SIVAI	Q02839 simian immu
733	37	40.2	1247	1 NOS_ANOST	Q16508 anopheles s	806	36	39.1	147	2	Q4XXJ9 PLACH	Q4xxj9 plasmodium
734	37	40.2	1259	2 Q9W061 DROME	Q9w061 drosophila	807	36	39.1	147	2	Q7NV70 PHOLL	Q7nv70 photorhabdu
735	37	40.2	1261	2 Q96685 DROME	Q96685 drosophila	808	36	39.1	151	1	LECT2_BOVIN	Q62644 bos taurus
736	37	40.2	1280	2 Q95RC8 DROME	Q95rc8 drosophila	809	36	39.1	164	2	Q34331 BACSU	Q34331 bacillus eu
737	37	40.2	1379	2 Q5WRU3 CAEBL	Q5wru3 caenorhabdi	810	36	39.1	173	2	Q5TG84 HUMAN	Q5tg84 homo sapien
738	37	40.2	1390	2 Q4KPH4 9VIRU	Q4kph4 bacterioph	811	36	39.1	173	2	Q6W80 CAEBR	Q6w80 caenorhabdi
739	37	40.2	1396	2 Q4HP70 GIBZE	Q4hpc7 gibberella	812	36	39.1	179	1	YB70 CAEBL	Q21045 caenorhabdi
740	37	40.2	1509	2 Q4P7F0 USTLAG	Q4p7f0 ustilago ma	813	36	39.1	179	1	Q5YZX3 NOCFA	Q5yzx3 nocardia fa
741	37	40.2	1633	1 YP74 CAEBL	Q09221 caenorhabdi	814	36	39.1	180	2	Q9RAJ2 MYCSX	Q9raj2 mycobacteri
742	37	40.2	2022	2 Q4T342 TETNG	Q4t342 tetraodon n	815	36	39.1	183	2	Q9KB28 BACHD	Q9kb28 bacillus ha
743	37	40.2	2039	2 Q4SJV2 TETNG	Q4sjv2 tetraodon n	816	36	39.1	186	2	Q5E5E1 VIBF1	Q5ese1 vibrio fisc
744	37	40.2	2143	2 Q9C8A6 ARATH	Q9c8a6 arabidopsis	817	36	39.1	186	2	Q69044 RHOPR	Q69044 rhodococcu
745	37	40.2	2151	2 Q8RVL2 ARATH	Q8rvl2 arabidopsis	818	36	39.1	186	2	Q6LLB6 PHOPR	Q6lllb6 photobacter
746	37	40.2	2209	2 Q4QEP0 LEIMA	Q4qep0 leishmania	819	36	39.1	190	2	Q6SH00 BACHD	Q6sh00 bacillus l1
747	37	40.2	2510	2 Q94658 PLAPA	Q94658 plasmodium	820	36	39.1	193	2	Q8NOF8 PLAVI	Q8nof8 plasmodium
748	37	40.2	2524	2 Q6C8Q9 YARLI	Q6c8q9 yarrowia li	821	36	39.1	196	2	Q8WVH4 MACMU	Q8wmh4 macaca mula
749	37	40.2	2544	2 Q4LY33 9BURK	Q4ly33 burkholderi	822	36	39.1	198	2	Q19147 CAEBL	Q19147 caenorhabdi
750	37	40.2	4034	2 Q5WRU2 CAEBL	Q5wru2 caenorhabdi	823	36	39.1	201	1	PYRP THEMEA	Q9wyg7 thermotoga
751	37	40.2	4862	2 Q5RI27 BRARE	Q5ri27 brachydanio	824	36	39.1	201	2	Q9ZSH3 RHIME	Q9zsh3 rhizobium m
752	37	40.2	4910	2 Q4SFN5 TETNG	Q4sfns tetraodon n	825	36	39.1	202	2	Q4ZS35 PSEES	Q4zs35 pseudomonas
753	37	40.2	5035	1 RYR1_PIG	P16960 sus scrofa	826	36	39.1	202	2	Q880L8 PSEES	Q880l8 pseudomonas
754	37	40.2	5035	2 Q29104_PIG	Q29104 sus scrofa	827	36	39.1	202	2	Q4KC17_PSEFS	Q4kc17 streptomyces
755	37	40.2	5035	2 Q29105_PIG	Q29105 sus scrofa	828	36	39.1	203	2	Q8CK56 STRCO	Q8ck56 streptomyces
756	37	40.2	5035	2 Q8OX16 MOUSE	Q8ox16 mus musculu	829	36	39.1	216	2	Q692L1_YEEN	Q692l1 yersinia en
757	37	40.2	5037	1 RYR1_RABIT	PL1716 cryptotagus	830	36	39.1	216	2	Q7W9I3_WOLSU	Q7w9i3 wolinnella s
758	37	40.2	5037	2 Q91313 RANCA	Q91313 rana catesb	831	36	39.1	221	2	Q7RYB1 NEUCR	Q7ryb1 neurospora
759	37	40.2	5038	1 RYR1_HUMAN	P21817 homo sapien	832	36	39.1	227	2	Q8WMH3 MACMU	Q8wmh3 macaca mula
760	37	40.2	5081	2 Q13054 MAKNI	Q13054 makaira nig	833	36	39.1	243	1	NCAP_PTPV	P03515 punta toro
761	37	40.2	7548	2 Q5WRU1 CAEBL	Q5wru1 caenorhabdi	834	36	39.1	243	1		

835	36	39.1	244	2	Q9BIX0_TRIPS	Q9bix0 trichinella	908	36	39.1	391	2	Q5VIX5_9RHAB	Q5vix5 infectious
836	36	39.1	245	2	Q73PD9_TREDE	Q73pd9 treponema d	909	36	39.1	391	2	Q5VIX6_9RHAB	Q5vix6 infectious
837	36	39.1	250	2	Q72N27_LEPIC	Q72n27 leptospira	910	36	39.1	391	2	Q5VIX7_9RHAB	Q5vix7 infectious
838	36	39.1	250	2	Q8F8J7_LEPTIN	Q8f8j7 leptospira	911	36	39.1	391	2	Q5VIY0_9RHAB	Q5viy0 infectious
839	36	39.1	254	2	Q4IAV9_GIBZE	Q4iav9 gibberella	912	36	39.1	391	2	Q5VIY2_9RHAB	Q5viy2 infectious
840	36	39.1	256	2	Q90LS7_9HIV1	Q90ls7 human immun	913	36	39.1	391	2	Q5VJ82_9RHAB	Q5vj82 infectious
841	36	39.1	257	2	Q6GOM7_BRARE	Q6gom7 brachydanio	914	36	39.1	391	2	Q68M50_9RHAB	Q68m50 infectious
842	36	39.1	262	2	Q8UIP0_AGR75	Q8uiip0 agrobacteri	915	36	39.1	391	2	Q82679_9RHAB	Q82679 infectious
843	36	39.1	262	2	Q98JQ3_RHILO	Q98jq3 rhizobium l	916	36	39.1	391	2	Q82680_9RHAB	Q82680 infectious
844	36	39.1	263	2	Q9HUX4_PSEAE	Q9hux4 pseudomonas	917	36	39.1	391	2	Q88449_9RHAB	Q88449 infectious
845	36	39.1	264	2	Q82924_STRAW	Q82924 streptomyc	918	36	39.1	394	1	PEPA_ASPAW	P17946 aspergillus
846	36	39.1	265	1	MUR12_BACSU	Q05412 bacillus su	919	36	39.1	394	2	P78735_PENJA	P78735 penicillium
847	36	39.1	265	2	Q6L875_BACSU	Q6l875 bacillus su	920	36	39.1	394	2	Q00207_ASPNG	Q00207 aspergillus
848	36	39.1	266	2	Q49712_ARATH	Q49712 arabidopsis	921	36	39.1	394	2	Q62153_CAENHAB1	Q62153 caenorhabd1
849	36	39.1	269	2	Q70681_PSEPU	Q70681 pseudomonas	922	36	39.1	396	2	Q63Y71_BURPS	Q63y71 burkholderi
850	36	39.1	272	2	Q514X6_ENTHI	Q514x6 entamoeba h	923	36	39.1	399	2	Q5LAF4_BACFN	Q5laf4 bacteroides
851	36	39.1	272	2	Q7DIU7_AGR75	Q7diu7 agrobacteri	924	36	39.1	399	2	Q8CX74_OCBIH	Q8cx74 oceanobacil
852	36	39.1	277	2	Q8G5M8_BIFLO	Q8g5m8 bifidobacte	925	36	39.1	401	2	Q515B6_ENTHI	Q515b6 entamoeba h
853	36	39.1	284	1	CI042_CHICK	Q52in7 gallus gall	926	36	39.1	406	1	YNQ5_YEAST	Y53891 saccharomyc
854	36	39.1	288	2	Q9KAB6_BACHD	Q9kab6 bacillus ha	927	36	39.1	409	2	Q72N67_LEPIC	Q72n67 leptospira
855	36	39.1	289	2	Q8FGB4_ECOL6	Q8fgb4 escherichia	928	36	39.1	409	2	Q8F8E6_LEPIN	Q8f8e6 leptospira
856	36	39.1	293	2	Q57IF1_SALCH	Q57if1 salmonella	929	36	39.1	410	2	Q62EN6_BURMA	Q62en6 burkholderi
857	36	39.1	293	2	Q5PLO4_SALPA	Q5plq4 salmonella	930	36	39.1	413	1	NCAP_IHNV	P19591 infectious
858	36	39.1	293	2	Q822D6_SALTI	Q8z2d6 salmonella	931	36	39.1	415	2	Q8KZG2_HELPI	Q8kzg2 helicobacte
859	36	39.1	293	2	Q8ZL71_SALTY	Q8z171 salmonella	932	36	39.1	416	2	Q6YRP4_SYNY3	Q6yrp4 synecocyst
860	36	39.1	293	2	Q7UBM8_SYNPX	Q7ubm8 synecococc	933	36	39.1	419	1	YLBE_ECOLI	Y87129 escherichia
861	36	39.1	298	2	Q6TUG7_RAT	Q6tug7 rattus norv	934	36	39.1	419	2	Q8FK53_ECOL6	Q8fk53 escherichia
862	36	39.1	300	2	Q961J0_HUMAN	Q961j0 homo sapien	935	36	39.1	421	2	Q86TT5_HUMAN	Q86tt5 homo sapien
863	36	39.1	301	2	Q89UN9_BRAJA	Q89un9 bradyrhizob	936	36	39.1	423	2	Q8N9E2_HUMAN	Q8n9e2 homo sapien
864	36	39.1	304	2	Q7UFW7_RHOB	Q7ufw7 rhodopirell	937	36	39.1	425	1	SVH_BUGBP	P59482 buchnera ap
865	36	39.1	305	2	Q74G80_GEOSL	Q74g80 geobacter s	938	36	39.1	425	2	Q9XCC1_STRFR	Q9xccl1 streptomyc
866	36	39.1	307	1	GPDA_ANASP	Q8ywc2 anabaena ep	939	36	39.1	431	1	TYRI_SCHPO	Q60078 schizosacch
867	36	39.1	309	2	Q675T8_9UROC	Q675t8 oikopleura	940	36	39.1	438	2	Q4QKW2_HAEI8	Q4qkw2 haemophilus
868	36	39.1	309	2	Q9XIP5_ARATH	Q9xip5 arabidopsis	941	36	39.1	442	1	NRX1B_HUMAN	P58400 homo sapien
869	36	39.1	309	2	Q6PH60_BRARE	Q6ph60 brachydanio	942	36	39.1	451	2	Q6LID0_PHOPR	Q6lid0 photobacter
870	36	39.1	311	2	Q8XHC8_CLOPE	Q8xhc8 clostridium	943	36	39.1	452	2	Q71LM1_TOBAC	Q71lm1 nicotiana t
871	36	39.1	312	2	Q5V2P3_HALMA	Q5v2p3 haloartula	944	36	39.1	453	1	NHAC_BACSU	Q07553 bacillus su
872	36	39.1	314	2	Q7X292_9ACTO	Q7x292 streptomyc	945	36	39.1	453	2	Q5KIX2_CRYNE	Q5kix2 cryptococcu
873	36	39.1	314	2	Q5KZD2_GEOKA	Q5kzd2 geobacillus	946	36	39.1	453	2	Q55TG5_CRYNE	Q55tg5 cryptococcu
874	36	39.1	319	2	Q6FY34_CANGA	Q6fy34 candida gla	947	36	39.1	454	2	Q4HXE1_GIBZE	Q4hxe1 gibberella
875	36	39.1	321	2	Q925Y0_RHIME	Q925y0 rhizobium m	948	36	39.1	455	2	Q88Z17_LACPE	Q88z17 lactobacill
876	36	39.1	321	2	Q92TH1_RHIME	Q92th1 rhizobium m	949	36	39.1	467	1	NRX1B_BOVIN	Q28142 bos taurus
877	36	39.1	322	2	Q6NWA1_BRARE	Q6nwa1 brachydanio	950	36	39.1	468	1	NRX1B_RAT	Q63373 rattus norv
878	36	39.1	323	2	Q54XQ5_DICDI	Q54xq5 dictyosteli	951	36	39.1	470	2	QSLIN5_BACFN	Q5slin5 bacteroides
879	36	39.1	327	2	Q4WSA7_BACCE	Q4wsa7 bacillus ce	952	36	39.1	470	2	Q4JT66_CORJK	Q4jt66 corynebacte
880	36	39.1	327	2	Q73BM0_BACC1	Q73bm0 bacillus ce	953	36	39.1	470	2	Q64ZS1_BACFR	Q64zsl1 bacteroides
881	36	39.1	329	2	Q9SUN8_ARATH	Q9sin8 arabidopsis	954	36	39.1	472	2	Q4SD76_TETNG	Q4sd76 tetraodon n
882	36	39.1	331	2	Q6HLQ9_BACHK	Q6hlq9 bacillus th	955	36	39.1	473	2	Q985G5_RHILO	Q985g5 rhizobium l
883	36	39.1	331	2	Q63E84_BACCZ	Q63e84 bacillus ce	956	36	39.1	475	1	FRIG_ERWCH	Q07162 erwania chr
884	36	39.1	331	2	Q5YVZ7_NOCPA	Q5yvz7 nocardia fa	957	36	39.1	486	2	Q4RU74_TETNG	Q4ru74 tetraodon n
885	36	39.1	333	2	Q8XCV6_ECO57	Q8xcv6 escherichia	958	36	39.1	488	2	Q76962_NASVI	Q76962 nasonia vit
886	36	39.1	335	2	Q623L3_CABBR	Q623l3 caenorhabd1	959	36	39.1	488	2	P72307_RHOOP	P72307 rhodococcu
887	36	39.1	335	2	Q829L9_STRAW	Q829l9 streptomyc	960	36	39.1	489	2	Q5CH47_CRYHO	Q5ch47 cryptospori
888	36	39.1	338	1	TISB_HUMAN	Q07352 homo sapien	961	36	39.1	490	1	AV77_YEAST	P40501 saccharomyc
889	36	39.1	338	1	TISB_MOUSE	P23950 mus musculu	962	36	39.1	504	2	O02254_CABEL	O02254 caenorhabd1
890	36	39.1	338	1	TISB_RAT	P17431 rattus norv	963	36	39.1	505	2	Q61L87_DROME	Q61l87 drosophila
891	36	39.1	338	2	Q91YI7_MOUSE	Q91yi7 mus musculu	964	36	39.1	511	2	Q86SX3_HUMAN	Q86sx3 homo sapien
892	36	39.1	338	2	Q543H2_MOUSE	Q543h2 m 9 days em	965	36	39.1	514	2	Q6T936_SALTU	Q6t936 salmo trutt
893	36	39.1	341	2	Q9UWE1_CANTR	Q9uwe1 candida tro	966	36	39.1	515	2	Q4RWI3_TETNG	Q4rwi3 tetraodon n
894	36	39.1	344	2	Q5XJ67_BRARE	Q5xj67 brachydanio	967	36	39.1	516	2	Q6NGR0_CORDI	Q6ngr0 corynebacte
895	36	39.1	348	2	Q8GXX6_ARATH	Q8gxx6 arabidopsis	968	36	39.1	522	2	Q8BGT5_MOUSE	Q8bgt5 m mus muscu
896	36	39.1	349	2	Q4NUC2_9DELT	Q4nuc2 anaeromyxob	969	36	39.1	522	2	Q8BVT7_MOUSE	Q8bvt7 mus musculu
897	36	39.1	352	2	Q67DX1_9ELAT	Q67dx1 ralatochia s	970	36	39.1	522	2	Q8KIJ3_MOUSE	Q8kij3 mus musculu
898	36	39.1	354	2	Q9AJY7_STRCO	Q9ajy7 streptomyc	971	36	39.1	522	2	Q5M7W3_RAT	Q5m7w3 rattus norv
899	36	39.1	355	2	Q51Q14_MAGGR	Q51q14 magnaporthe	972	36	39.1	523	2	Q8TD30_HUMAN	Q8td30 homo sapien
900	36	39.1	358	2	Q7VF36_HELHP	Q7vf36 helicobacte	973	36	39.1	524	1	PPBT_FELCA	Q29486 felis silve
901	36	39.1	362	1	FABH2_VIBVU	Q8d719 vibrio vuln	974	36	39.1	529	1	NRX1A_MOUSE	Q9c884 mus musculu
902	36	39.1	362	1	FABH2_VIBVU	Q7m713 vibrio vuln	975	36	39.1	533	2	Q5BFG7_EMENI	Q5bfg7 aspergillus
903	36	39.1	362	2	Q4FWV0_LEIMA	Q4fwv0 leishmania	976	36	39.1	533	2	Q4WCS0_ASPFU	Q4wcs0 aspergillus
904	36	39.1	379	2	Q34599_BACSU	Q34599 bacillus su	977	36	39.1	534	2	Q9LLE1_TOBAC	Q9lle1 nicotiana t
905	36	39.1	387	2	Q8STL9_ENCCU	Q8stl9 encephalito	978	36	39.1	538	2	Q967D0_GEOCY	Q967d0 geodia cydo
906	36	39.1	391	2	Q5VIX1_9RHAB	Q5vix1 infectious	979	36	39.1	547	2	P97531_RAT	P97531 rattus norv
907	36	39.1	391	2	Q5VIX2_9RHAB	Q5vix2 infectious	980	36	39.1	547	2	Q6P744_RAT	Q6p744 rattus norv

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981 36 39.1 548 2 Q5XQP1 9SACH
982 36 39.1 548 2 Q7N484 PHOLL
983 36 39.1 551 2 Q8UAQ1 AGRTS
984 36 39.1 556 2 Q6FS53 CANGA
985 36 39.1 560 1 CBS RAT
986 36 39.1 560 2 Q7ZUX0 BRARE
987 36 39.1 564 2 Q9UFA0 HUMAN
988 36 39.1 565 2 Q6C5H1 YARLI
989 36 39.1 567 2 Q6FMJ8 CANGA
990 36 39.1 569 2 Q54PS7 DICDI
991 36 39.1 569 2 Q84K25 ARATH
992 36 39.1 569 2 Q8LCN9 ARATH
993 36 39.1 573 2 Q8DM18 SYNEL
994 36 39.1 577 2 Q5AS59 EMENI
995 36 39.1 579 2 Q9US10 SCHPO
996 36 39.1 579 2 Q8LDL2 ARATH
997 36 39.1 579 2 Q9SRK7 ARATH
998 36 39.1 582 2 Q8R5J8 MOUSE
999 36 39.1 592 1 GCL_ECOLI
1000 36 39.1 592 2 Q8TNU9 METAC

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ALIGNMENTS

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RESULT 1
ANFB HUMAN
ID ANFB HUMAN STANDARD; PRT; 134 AA.
AC P16960;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-WAY-2005 (Rel. 47, Last annotation update)
DE Natriuretic peptides B precursor [Contains: Gamma-brain natriuretic
DE peptide; Brain natriuretic peptide 32 (BNP-32)].
GN Name-NPPB;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90088474; PubMed=2597152;
RA Seilhamer J.J., Arfsten A., Miller J.A., Lundquist P.,
RA Scarborough R.M., Lewicki J.A., Porter J.G.;
RT "Human and canine gene homologs of porcine brain natriuretic
RT peptide.";
RL Biochem. Biophys. Res. Commun. 165:650-658(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89193743; PubMed=2522777;
RA Sudoh T., Maekawa K., Kojima M., Minamino N., Kangawa K., Matsuo H.;
RT "Cloning and sequence analysis of cDNA encoding a precursor for human
RT brain natriuretic peptide.";
RL Biochem. Biophys. Res. Commun. 159:1427-1434(1989).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG Human chromosome 1 international sequencing consortium;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP PROTEIN SEQUENCE OF 27-58 AND 103-134.
RX MEDLINE=90211249; PubMed=2138890;
RA Hino J., Tateyaa H., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation and identification of human brain natriuretic peptides in
RT cardiac atrium.";
RL Biochem. Biophys. Res. Commun. 167:693-700(1990).
RN [6]
RP PROTEIN SEQUENCE OF 103-134.
RX MEDLINE=90092577; PubMed=2136732; DOI=10.1016/0014-5793(90)80043-J;
RA Kambayashi Y., Nakao K., Mukoyama M., Saito Y., Ogawa Y., Shiono S.,
RA Inouye K., Yoshida N., Imura H.;
RT "Isolation and sequence determination of human brain natriuretic
RT peptide in human atrium.";
RL FEBS Lett. 259:341-345(1990).
CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological
CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the
CC body's salt and water balance. Improves heart function.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Brain and also in atria, but at much lower
CC levels than ANP.
CC -!- PHARMACEUTICAL: Available under the name Nesiritide (Scios). Used
CC for the treatment of heart failure.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M31776; AAA35603.1; -; Genomic_DNA.
CC EMBL; M25296; AAA36355.1; -; mRNA.
CC EMBL; AL021155; CAA15956.1; -; Genomic_DNA.
CC EMBL; BC025785; AAH25785.1; -; mRNA.
CC FIR; A36736; AWHUB.
CC Ensembl; ENSG00000120937; Homo sapiens.
CC HGNC; HGNC:7940; NPPB.
CC H-InvDB; HIX0000131; -.
CC MIM; 600295; -.
CC GO; GO:0005615; C:extracellular space; NAS.
CC GO; GO:0008613; F:diuretic hormone activity; TAS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; NAS.
CC GO; GO:0030146; P:diuresis; TAS.
CC GO; GO:0007589; P:fluid secretion; TAS.
CC GO; GO:0030147; P:natriuresis; TAS.
CC GO; GO:0016525; P:negative regulation of cell growth; NAS.
CC GO; GO:0030308; P:negative regulation of blood pressure; NAS.
CC GO; GO:0008217; P:regulation of vascular permeability; TAS.
CC GO; GO:0043114; P:regulation of vasodilation; NAS.
CC GO; GO:0043312; P:regulation of vasodilation; NAS.
CC InterPro; IPR002408; Br_natriureticp.
CC InterPro; IPR000663; Natr_peptide.
CC Pfam; PF00212; ANP; 1.
CC PRINTS; PR00712; BNATPEPTIDE.
CC PRINTS; PR00710; NATPEPTIDES.
CC ProDom; PD005617; NATPEPTIDE; 1.
CC PROSITE; PS00263; NATRIURETIC PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Polymorphism; Signal; Vasoactive.
FT SIGNAL 1 26
FT CHAIN 27 134 Gamma-brain natriuretic peptide.

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FT PEPTIDE 103 134 Brain natriuretic peptide 32.
FT DISULFID 112 128 BY similarity.
FT VARIANT 25 25 R -> L (in dbSNP:5227) .
FT VARIANT 47 47 /FTId=VAR 014580.
FT VARIANT 47 47 R -> H (in dbSNP:5229) .
FT VARIANT 93 93 /FTId=VAR 014581.
FT VARIANT 93 93 M -> L (in dbSNP:5230) .
FT SEQUENCE 134 AA; 14726 MW; DC884D9408462146 CRC64;

Query Match 100.0%; Score 92; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | |
Db 112 CFGRKMDRISSSSGLGC 128

RESULT 2
ID Q6FGYO HUMAN PRELIMINARY; PRT; 134 AA.
AC Q6FGYO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE NPPB protein.
GN Name=NPPB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mkoondinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541976; CAG46774.1; -; mRNA.
DR EMBL; CR542003; CAG46800.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
KW Vasoactive.
SQ SEQUENCE 134 AA; 14726 MW; DC884D9408462146 CRC64;

Query Match 100.0%; Score 92; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | |
Db 112 CFGRKMDRISSSSGLGC 128

RESULT 3
ID ANFB BOVIN STANDARD; PRT; 103 AA.
AC P13204;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Natriuretic peptides B precursor [Contains: Gamma-brain natriuretic
DE peptide; Aldosterone secretion inhibitory factor (ASIF); Brain
DE natriuretic peptide 26 (BNP-26)].
GN Name=NPPB;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

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RP PROTEIN SEQUENCE.
RX MEDLINE=90114187; PubMed=2532709;
RA Nguyen T.T., Lazure C., Babinski K., Chretien M., de Lean A., Ong H.;
RT "Purification and primary structure of pro-aldoosterone secretion
RT inhibitory factor from bovine adrenal chromaffin cells.";
RL Mol. Endocrinol. 3:1823-1829(1989).
RN [2]
RP PROTEIN SEQUENCE OF 69-103.
RX MEDLINE=89136947; PubMed=2537187;
RA Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;
RT "Aldosterone secretion inhibitory factor: a novel neuropeptide in
RT bovine chromaffin cells.";
RL Endocrinology 124:1591-1593(1989).
CC -I- FUNCTION: Acts as a cardiac hormone with a variety of biological
CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the
CC body's salt and water balance. Improves heart function.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Brain and also in atria, but at much lower
CC levels than ANP.
CC -I- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A41403; A41403.
CC InterPro; IPR002408; Br_natriurtpep.
CC InterPro; IPR000663; Natr_peptide.
CC Pfam; PF00212; ANP; 1.
CC PRINTS; PR00712; BNATPEPTIDES.
CC PRINTS; PR00710; NATPEPTIDES.
CC ProDom; PD005617; Natr_peptide; 1.
CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Vasoactive.
FT CHAIN 1 103 Gamma-brain natriuretic peptide.
FT PEPTIDE 69 103 Aldosterone secretion inhibitory factor.
FT PEPTIDE 78 103 Brain natriuretic peptide 26.
FT DISULFID 81 97
SQ SEQUENCE 103 AA; 11249 MW; 40209204AFE3851D CRC64;

Query Match 82.6%; Score 76; DB 1; Length 103;
Best Local Similarity 76.5%; Pred. No. 3.6e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | |
Db 81 CFGRKMDRISSSSGLGC 97

RESULT 4
ID Q9GLK5_FELCA PRELIMINARY; PRT; 112 AA.
AC Q9GLK5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Brain natriuretic peptide (fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Liu Z.L., Wiedmeyer C.E., Solter P.F., Sisson D.D.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF251261; AAG13660.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.

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DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDES.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT NON_TER 1 1
FT NON_TER 112 112
FT SEQUENCE 112 AA; 12083 MW; 580224F12984FFB2 CRC64;
Query Match 82.6%; Score 76; DB 2; Length 112;
Best Local Similarity 76.5%; Pred. No. 3.9e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFGKQMDRISSSSGLGC 17
Db 90 CFGRLDRIGSLGLGC 106
RESULT 5
ANFC2_ORYLA STANDARD; PRT; 126 AA.
AC Q8AYR5;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-2 precursor.
GN Name=cnp-2;
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND SYNTHESIS.
RC TISSUE=Brain;
RA PubMed=12893874; DOI=10.1073/pnas.1632368100;
RT "Four functionally distinct C-type natriuretic peptides found in fish reveal evolutionary history of the natriuretic peptide system.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -!- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has CGMP-stimulating activity. May help to regulate body fluid homeostasis in a variety of aquatic environments.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Brain and spinal cord.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
DR EMBL; AB081456; BAC15761.1; -; mRNA.
DR InterPro; IPR002408; Br_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR Hormone; Signal; Vasoactive.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 100 By similarity.
FT PROPEP 103 126 C-type natriuretic peptide-2.
FT PEPTIDE 110 126 By similarity.
FT DISULFID 110 126
SQ SEQUENCE 112 AA; 12083 MW; 580224F12984FFB2 CRC64;
GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDES.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT NON_TER 1 1
FT NON_TER 112 112
FT SEQUENCE 112 AA; 12083 MW; 580224F12984FFB2 CRC64;
Query Match 82.6%; Score 76; DB 2; Length 112;
Best Local Similarity 76.5%; Pred. No. 3.9e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFGKQMDRISSSSGLGC 17
Db 90 CFGRLDRIGSLGLGC 106
RESULT 5
ANFC2_ORYLA STANDARD; PRT; 126 AA.
AC Q8AYR5;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-2 precursor.
GN Name=cnp-2;
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND SYNTHESIS.
RC TISSUE=Brain;
RA PubMed=12893874; DOI=10.1073/pnas.1632368100;
RT "Four functionally distinct C-type natriuretic peptides found in fish reveal evolutionary history of the natriuretic peptide system.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -!- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has CGMP-stimulating activity. May help to regulate body fluid homeostasis in a variety of aquatic environments.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Brain and spinal cord.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC -----
DR EMBL; AB081456; BAC15761.1; -; mRNA.
DR InterPro; IPR002408; Br_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR Hormone; Signal; Vasoactive.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 100 By similarity.
FT PROPEP 103 126 C-type natriuretic peptide-2.
FT PEPTIDE 110 126 By similarity.
FT DISULFID 110 126
SQ SEQUENCE 112 AA; 12083 MW; 580224F12984FFB2 CRC64;
SQ SEQUENCE 126 AA; 13400 MW; 9D5D7B8DDECB0F92 CRC64;
Query Match 82.6%; Score 76; DB 1; Length 126;
Best Local Similarity 82.4%; Pred. No. 4.4e-05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGKQMDRISSSSGLGC 17
Db 110 CFGKMDRIGSISGLGC 126
RESULT 6
ANFB_SHEEP STANDARD; PRT; 129 AA.
ID ANFB_SHEEP
AC O46541;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Natriuretic peptides B precursor [Contains: Gamma-brain natriuretic peptide; Brain natriuretic peptide 29 (BNP-29); Brain natriuretic peptide 26 (BNP-26)].
GN Name=NPPB;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99236261; PubMed=10219521; DOI=10.1016/S0739-7240(99)00005-3;
RA Aitken G.D., Raizis A.M., Yandle T.G., George P.M., Espiner E.A., Cameron V.A.;
RT "The characterization of ovine genes for atrial, brain, and C-type natriuretic peptides.";
RL Domest. Anim. Endocrinol. 16:115-121(1999).
CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological actions including natriuresis, diuresis, vasorelaxation, and inhibition of renin and aldosterone secretion. It is thought to play a key role in cardiovascular homeostasis. Helps restore the body's salt and water balance. Improves heart function.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC -----
DR EMBL; AF037466; AAB92565.1; -; Genomic_DNA.
DR InterPro; IPR002408; Br_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR Hormone; Signal; Vasoactive.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 129 Gamma-brain natriuretic peptide.
FT PEPTIDE 101 129 Brain natriuretic peptide 29 (By similarity).
FT PEPTIDE 104 129 Brain natriuretic peptide 26 (By similarity).
FT DISULFID 107 123 By similarity.
FT SEQUENCE 129 AA; 14118 MW; 13D4DF91D32A28EF CRC64;
Query Match 82.6%; Score 76; DB 1; Length 129;
Best Local Similarity 76.5%; Pred. No. 4.6e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFGKQMDRISSSSGLGC 17
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Db      107  CFGRRLDRIGSLGLGC 123
||||:|||||
RESULT 7
ANFB_PIG STANDARD; PRT; 131 AA.
ID ANFB_PIG STANDARD; PRT; 131 AA.
AC P07634;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Natriuretic peptides B precursor [Contains: Gamma-brain natriuretic
DE peptide; Brain natriuretic peptide 32 (BNP-32); Brain natriuretic
DE peptide 26 (BNP-26)].
GN Names: NPPB;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89061744; PubMed=3196348;
RA Maekawa K., Sudoh T., Furusawa M., Minamino N., Kangawa K., Okhubo H.,
RA Nakanishi S., Matsuo H.;
RT "Cloning and sequence analysis of cDNA encoding a precursor for
RT porcine brain natriuretic peptide."
RL Biochem. Biophys. Res. Commun. 157:410-416(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89214071; PubMed=2708334;
RA Porter J.G., Arfsten A., Falisi T., Scarborough R.M., Lewicki J.A.,
RA Seilhamer J.J.;
RT "Cloning of a cDNA encoding porcine brain natriuretic peptide."
RL J. Biol. Chem. 264:6689-6692(1989).
RN [3]
RP PROTEIN SEQUENCE OF 26-131.
RX MEDLINE=89061743; PubMed=3196347;
RA Minamino N., Kangawa K., Matsuo H.;
RT "Isolation and identification of a high molecular weight brain
RT natriuretic peptide in porcine cardiac atrium."
RL Biochem. Biophys. Res. Commun. 157:402-409(1988).
RN [4]
RP PROTEIN SEQUENCE OF 100-131.
RX MEDLINE=88339957; PubMed=3421965;
RA Sudoh T., Minamino N., Kangawa K., Matsuo H.;
RT "Brain natriuretic peptide-32: N-terminal six amino acid extended form
RT of brain natriuretic peptide identified in porcine brain."
RL Biochem. Biophys. Res. Commun. 155:726-732(1988).
RN [5]
RP PROTEIN SEQUENCE OF 106-131.
RX MEDLINE=88156915; PubMed=2964562; DOI=10.1038/332078a0;
RA Sudoh T., Kangawa K., Minamino N., Matsuo H.;
RT "A new natriuretic peptide in porcine brain."
RL Nature 332:78-81(1988).
RN [6]
RP STRUCTURE BY NMR OF BNP-26.
RX MEDLINE=91031435; PubMed=2146114;
RA Inooka H., Kikuchi T., Endo S., Ishibashi Y., Wakimasu M., Mizuta E.;
RT "Conformation in solution of porcine brain natriuretic peptide
RT determined by combined use of nuclear magnetic resonance and distance
RT geometry."
RL Eur. J. Biochem. 193:127-134(1990).
RN [7]
RP STRUCTURE BY NMR OF BNP-32.
RX MEDLINE=92007873; PubMed=1915362;
RA Craik D., Munro S., Nielsen K., Shehan P., Tregear G., Wade J.;
RT "The conformation of porcine brain natriuretic peptide by two-
RT dimensional NMR spectroscopy."
RL Eur. J. Biochem. 201:183-191(1991).
CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological
CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the

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CC play a key role in cardiovascular homeostasis. Helps restore the
CC body's salt and water balance. Improves heart function.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Brain and also in atria, but at much lower
CC levels than ANP.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M23596; AAB59258.1; -; mRNA.
CC EMBL; M25547; AAA31007.1; -; Genomic_DNA.
CC PIR; A31676; A31676.
CC PIR; A33873; A33873.
CC InterPro; IPR002408; Br_natriurtpep.
CC InterPro; IPR000663; Natr_peptide.
CC Pfam; PF00212; ANP; 1.
CC PRINTS; PR00712; ENATPEPTIDE.
CC PRINTS; PR00710; NATPEPTIDES.
CC ProDom; PD005617; Natr_peptide; 1.
CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
CC Direct protein sequencing; Hormone; Signal; Vasoactive.
KW SIGNAL 1 25
FT CHAIN 26 131 Gamma-brain natriuretic peptide.
FT PEPTIDE 100 131 Brain natriuretic peptide 32.
FT PEPTIDE 106 131 Brain natriuretic peptide 26.
FT DISULFID 109 125
FT VARIANT 26 26 H -> Y (in a clone).
SQ SEQUENCE 131 AA; 14512 MW; CC2F6E6E4A50C18A CRC64;

Query Match 82.6%; Score 76; DB 1; Length 131;
Best Local Similarity 76.5%; Pred. No. 4.6e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGLGC 17
|||:|||||
Db 109 CFGRRLDRIGSLGLGC 125

RESULT 8
ANFB_FELCA STANDARD; PRT; 132 AA.
ID ANFB_FELCA STANDARD; PRT; 132 AA.
AC Q9GLK4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Natriuretic peptides B precursor [Contains: Gamma-brain natriuretic
DE peptide; Brain natriuretic peptide 32 (BNP-32)].
GN Name=NPPB; Synonyms=BNP;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart atrium;
RX MEDLINE=22114979; PubMed=12119112; DOI=10.1016/S0378-1119(02)00676-5;
RA Liu Z.L., Wiedmeyer C.E., Sisson D.D., Solter P.F.;
RT "Cloning and characterization of feline brain natriuretic peptide."
RL Gene 292:183-190(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Liu Z.L.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological
CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the

```

CC body's salt and water balance. Improves heart function (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF253495; AAG13661.1; -; mRNA.
CC EMBL; AF425738; AAL24812.1; -; Genomic_DNA.
CC InterPro; IPR002408; Br_natriurtcpep.
CC InterPro; IPR000663; Natr_peptide.
CC Pfam; PF00212; ANP; 1.
CC PRINTS; PR00712; NATPEPTIDES.
CC PRODOM; PD005617; Natr_peptide; 1.
CC SMART; SM00183; NAT_PEP; 1.
CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 26 By similarity.
FT CHAIN 27 132 Gamma-brain natriuretic peptide.
FT PEPTIDE 101 132 Brain natriuretic peptide 32 (By
FT similarity).
FT DISULFID 110 126 By similarity.
FT SEQUENCE 132 AA; 14344 MW; D069B5F76A6C3510 CRC64;
Query Match 82.6%; Score 76; DB 1; Length 132;
Best Local Similarity 76.5%; Pred. No. 4.7e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 110 CFGRRLDRIGSLGSLGC 126

RESULT 9
Q6L723 CAMDR PRELIMINARY; PRT; 132 AA.
AC Q6L723;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE B-type natriuretic peptide precursor.
GN Name-BNP;
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Tylopoda;
OC Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Heart;
RA Oeman A.H.K., Yuge S., Hyodo S., Sato S., Maeda S., Marie H.,
RA Caceci T., Birkawa N., Naruse K., Naruse M., Takei Y.;
RT "Molecular identification and immunohistochemical localization of
RT atrial natriuretic peptide in the heart of the dromedary camel
RT (Camelus dromedarius).";
RL Comp. Biochem. Physiol., Part A Mol. Integr. Physiol.
RL 139:417-424 (2004).
DR EMBL; AB127392; BAD21300.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; P:hormone activity; IEA.
DR GO; GO:0005080; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; NATPEPTIDES.
DR PRODOM; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.

DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Signal; Vasoactive. 26 Potential.
FT SIGNAL 1 26
SQ SEQUENCE 132 AA; 14600 MW; 86B4094542A3E39E CRC64;
Query Match 82.6%; Score 76; DB 2; Length 132;
Best Local Similarity 76.5%; Pred. No. 4.7e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 110 CFGRRLDRIGSLGSLGC 126

RESULT 10
ANFB CANFA STANDARD; PRT; 140 AA.
AC ANFB CANFA
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Natriuretic peptides B precursor [Contains: Gamma-brain natriuretic
DE peptide; Brain natriuretic peptide 34 (BNP-34); Brain natriuretic
DE peptide 29 (BNP-29)].
GN Name-NPFB;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90088474; PubMed=2597152;
RA Seilhamer J.J., Arfsten A., Miller J.A., Lundquist P.,
RA Scarborough R.M., Lewicki J.A., Porter J.G.;
RT "Human and canine gene homologs of porcine brain natriuretic
RT peptide.";
RL Biochem. Biophys. Res. Commun. 165:650-658 (1989).
CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological
CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the
CC body's salt and water balance. Improves heart function.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Brain and also in atria, but at much lower
CC levels than ANP.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M31777; AAA30832.1; -; Genomic_DNA.
CC FIR; B36736; B36736.
CC Ensembl; ENSCARG00000016538; Canis familiaris.
CC InterPro; IPR002408; Br_natriurtcpep.
CC InterPro; IPR000663; Natr_peptide.
CC Pfam; PF00212; ANP; 1.
CC PRINTS; PR00712; NATPEPTIDES.
CC PRINTS; PR00710; NATPEPTIDES.
CC PRODOM; PD005617; Natr_peptide; 1.
CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 140 Gamma-brain natriuretic peptide.
FT PEPTIDE 107 140 Brain natriuretic peptide 34.
FT PEPTIDE 112 140 Brain natriuretic peptide 29.
FT DISULFID 118 134 By similarity.
FT SEQUENCE 140 AA; 14966 MW; 612B86F4D0FD49D9 CRC64;
Query Match 82.6%; Score 76; DB 1; Length 140;


```
Best Local Similarity 76.5%; Pred. No. 5e-05; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 2;

QY 1 CFGRKMDRISSSGLGC 17
Db 118 CFGRLDRIGSLGLGC 134

RESULT 11
Q7T217 ONCMY
ID Q7T217 ONCMY PRELIMINARY; PRT; 146 AA.
AC Q7T217;
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Atrial natriuretic peptide.
GN Name=anp;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Inoue K., Russel M.J., Olson K.R., Takei Y.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB076603; BAC77769.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological process; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002407; At_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; ANATPEPTIDE.
DR PRODOM; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 146 AA; 16043 MW; FED2CB3C79121BD0 CRC64;

Query Match 82.6%; Score 76; DB 2; Length 146;
Best Local Similarity 76.5%; Pred. No. 5.2e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSGLGC 17
Db 124 CFGARMDRIGTSSGLGC 140

RESULT 12
Q78AW6 SALSA
ID Q78AW6 SALSA PRELIMINARY; PRT; 148 AA.
AC Q78AW6;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Cardiac peptide precursor.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=20114377; PubMed=10650955; DOI=10.1210/en.141.2.731;
RX Majalahti-Paivainen T., Hirvonen M., Tervonen V., Ilves M.,
RA Ruskoaho H., Vuolteenaho O.;
RT "Gene structure of a new cardiac peptide hormone: a model for heart-
specific gene expression.";
RN Endocrinology 141:731-740(2000).
[2]
```

```
RP NUCLEOTIDE SEQUENCE.
RA Vuolteenaho O.J.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006421; CAA07023.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological process; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002407; At_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; ANATPEPTIDE.
DR PRODOM; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Signal; Vasoactive.
FT SIGNAL 1 119 Potential.
FT CHAIN 120 148 cardiac peptide.
SQ SEQUENCE 148 AA; 16236 MW; 934985642C25C739 CRC64;

Query Match 82.6%; Score 76; DB 2; Length 148;
Best Local Similarity 76.5%; Pred. No. 5.3e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSGLGC 17
Db 126 CFGARMDRIGTSSGLGC 142

RESULT 13
Q9YGVJ SALSA
ID Q9YGVJ SALSA PRELIMINARY; PRT; 152 AA.
AC Q9YGVJ;
DT 01-MAY-1999 (TREMELrel. 10, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Cardiac hormone.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tervonen V., Arjamaa O., Ruskoaho H., Vuolteenaho O.;
RT "New vasoactive cardiac hormone released by mechanical load.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RA Vuolteenaho O.J.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ001806; CAA05022.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological process; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002407; At_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; ANATPEPTIDE.
DR PRODOM; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT CHAIN 124 152 cardiac hormone.
SQ SEQUENCE 152 AA; 16740 MW; EID3E38A159CFEEA CRC64;

Query Match 82.6%; Score 76; DB 2; Length 152;
Best Local Similarity 76.5%; Pred. No. 5.4e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

QY 1 CFCGRMDRISSSSGLGC 17
||| :||| :|||
Db 130 CFCGRMDRIGTSSSGLGC 146

RESULT 14
NFNP_PSEPC STANDARD; PRT; 37 AA.
AC P82972;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Natriuretic peptide PNP.
OS Pseudocerastes persicus (Persian horned viper) (False horned viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Pseudocerastes.
OX NCBI_TaxID=47769;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, MASS SPECTROMETRY, AND DISULFIDE BOND.
RC TISSUE=Venom;
RX PubMed=14741349; DOI=10.1016/S0014-5793(03)01455-8;
RA Aminiasab M., Elmi M.M., Endlich N., Endlich K., Parekh N.,
RA Naderi-Manesh H., Schaller J., Mostafavi H., Sattler M.,
RA Sarbolouki M.N., Muhle-Goll C.;
RT "Functional and structural characterization of a novel member of the
RT natriuretic family of peptides from the venom of Pseudocerastes
RT persicus";
RL FEBS Lett. 557:104-108(2004).
CC -!- FUNCTION: Increases urine flow and decreases blood pressure when
CC administered to rats by intravenous injection. Inhibits thrombin-
CC induced platelet aggregation. Has a cGMP-stimulating activity.
CC -!- SUBUNIT: Monomer. Binds to the NPR-A receptor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=3941.5; MW_ERR=0.17; METHOD=Electrospray;
CC RANGE=1-37; NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC GO: GO:0005576; C:extracellular region; IDA.
CC GO: GO:0030146; P:diuresis; IDA.
CC GO: GO:0045776; P:negative regulation of blood pressure; IDA.
CC GO: GO:0009405; P:pathogenesis; IDA.
CC GO: GO:0030828; P:positive regulation of cGMP biosynthesis; IDA.
CC InterPro; IPR002407; At_natriurtcp.
CC InterPro; IPR002408; Br_natriurtcp.
CC InterPro; IPR000663; Natr_peptide.
CC Pfam; PF00212; ANP; 1.
CC PRINTS; PR00712; BNATPEPTIDE.
CC PRINTS; PR00710; NATPEPTIDES.
CC ProDom; PD005107; At_natriurtcp; 1.
CC ProDom; PD005617; Natr_peptide; 1.
CC SMART; SM00183; NAT_PEP; 1.
CC PROSITE; PS00263; NATRIURETIC_PPTIDE; 1.
CC Direct protein sequencing; Toxin; Vasoactive.
FT DISULFID 14 30
SQ SEQUENCE 37 AA; 3944 MW; AD7BE649AD480BA6 CRC64;

Query Match 80.4%; Score 74; DB 1; Length 37;
Best Local Similarity 76.5%; Pred. No. 2.8e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFCGRMDRISSSSGLGC 17
||| :||| :|||
Db 14 CFCGRMDRIGTSSSGLGC 30

RESULT 15
Q7LZ09_VIPLE PRELIMINARY; PRT; 38 AA.
AC Q7LZ09;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Lebetin 2 isoform alpha.
OS Vipera lebetina (Elephant snake) (Leventine viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Macrovipera.
OX NCBI_TaxID=8709;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96354866; PubMed=8769304; DOI=10.1016/0014-5793(96)00774-0;
RA Barbouche R., Marzachi N., Mansuelle P., Krifi M., Fenouillet E.,
RA Rochat H., El Ayeub M.;
RT "Novel anti-platelet aggregation polypeptides from Vipera lebetina
RT venom: isolation and characterization.";
RL FEBS Lett. 392:6-10(1996).

DR PIR; S71381; S71381.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0005080; P:regulation of blood vessel size; IEA.

DR InterPro; IPR002408; Br_natriurtcp.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.

DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.

DR PROSITE; PS00263; NATRIURETIC_PPTIDE; 1.
KW Vasoactive.

SQ SEQUENCE 38 AA; 3945 MW; 831FA5C9B1B09377 CRC64;

Query Match 80.4%; Score 74; DB 2; Length 38;
Best Local Similarity 76.5%; Pred. No. 2.9e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFCGRMDRISSSSGLGC 17
||| :||| :|||
Db 14 CFCGRMDRIGTSSSGLGC 30

RESULT 16

Q4TD23_TETNG PRELIMINARY; PRT; 83 AA.
AC Q4TD23;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAR6568, whole genome shotgun sequence.
DE (Fragment).
GN ORFName=GSTENG0003028001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]

NUCLEOTIDE SEQUENCE.
RP Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chaplier C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAE01006568; CAF89209.1; -; Genomic_DNA.
 DR InterPro; IPR002408; Br_natriurtcpep.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00712; BNATPEPTIDES.
 DR PRODOM; PD005617; Natr_peptide; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Vasoactive.
 FT NON TER 83 83
 SQ SEQUENCE 83 AA; 9432 MW; 5D020DD1512E2DF6 CRC64;
 Query Match 80.4%; Score 74; DB 2; Length 83;
 Best Local Similarity 76.5%; Pred. No. 6.5e-05;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFGKMDRISSSSLGQC 17
 DB 65 CFGRRMDRIGSMSSSLGC 81
 RESULT 17
 ANFB_FUGRU
 ID ANFB_FUGRU STANDARD; PRT; 133 AA.
 AC Q805D7;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Brain natriuretic peptide precursor (B-type natriuretic peptide).
 GN Name=BNP;
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Heart;
 RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
 RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
 RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
 RT sturgeon: identification of BNP in fish lineage.";
 RL J. Mol. Endocrinol. 32:547-555(2004).
 CC -1- FUNCTION: Acts as a cardiac hormone with a variety of biological
 CC actions including natriuresis, diuresis, vasorelaxation, and
 CC inhibition of renin and aldosterone secretion. It is thought to
 CC play a key role in cardiovascular homeostasis. Helps restore the
 CC body's salt and water balance. Improves heart function.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AB089934; BAC57070.1; -; mRNA.
 DR Ensembl; SINFUG000000135753; Fugu rubripes.

DR InterPro; IPR002408; Br_natriurtcpep.
 DR InterPro; IPR000663; Natr_peptide.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00712; BNATPEPTIDES.
 DR PRODOM; PD005617; Natr_peptide; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Hormone; Signal; Vasoactive.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 ?
 FT PEPTIDE ? 133 Brain natriuretic peptide.
 FT DISULFID 108 124 By similarity.
 SQ SEQUENCE 133 AA; 14746 MW; FD4541B255A33436 CRC64;
 Query Match 80.4%; Score 74; DB 1; Length 133;
 Best Local Similarity 76.5%; Pred. No. 0.00011;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFGKMDRISSSSLGQC 17
 DB 108 CFGRRMDRIGSMSSSLGC 124
 RESULT 18
 ANFB_OREMO
 ID ANFB_OREMO STANDARD; PRT; 138 AA.
 AC Q805E8;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Brain natriuretic peptide precursor (B-type natriuretic peptide).
 GN Name=BNP;
 OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidae;
 OC Cichlidae; African cichlids; Pseudocrenilabrinae; Tilapini;
 OC Oreochromis.
 OX NCBI_TaxID=8127;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Heart;
 RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
 RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
 RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
 RT sturgeon: identification of BNP in fish lineage.";
 RL J. Mol. Endocrinol. 32:547-555(2004).
 CC -1- FUNCTION: Acts as a cardiac hormone with a variety of biological
 CC actions including natriuresis, diuresis, vasorelaxation, and
 CC inhibition of renin and aldosterone secretion. It is thought to
 CC play a key role in cardiovascular homeostasis. Helps restore the
 CC body's salt and water balance. Improves heart function.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AB087284; BAC55025.1; -; mRNA.
 DR InterPro; IPR002408; Br_natriurtcpep.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00712; BNATPEPTIDES.
 DR PRODOM; PD005617; Natr_peptide; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Hormone; Signal; Vasoactive.
 FT SIGNAL 1 22 Potential.

```
FT PROPEP      23      ?
FT PEPTIDE     111      ? 138 Brain natriuretic peptide.
FT DISULFID    111      ? 127 By similarity.
SQ SEQUENCE    138 AA; 15189 MW; 5A023AB1F4F452FA CRC64;

Query Match      80.4%; Score 74; DB 1; Length 138;
Best Local Similarity 76.5%; Pred. No. 0.00011;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGCG 17
    |||||:|||||
Db 111 CFGRKMDRIGSMSSSLGCG 127

RESULT 19
Q7TIQ2 ORYLA
ID Q7TIQ2_ ORYLA PRELIMINARY; PRT; 146 AA.
AC Q7TIQ2_
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE B-type natriuretic peptide.
GN Name=bnp;
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA Inoue K., Takei Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB099700; BAC79151.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002406; C_natriureticpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 146 AA; 16455 MW; E0EA2C0C70DAD51F CRC64;

Query Match      80.4%; Score 74; DB 2; Length 146;
Best Local Similarity 76.5%; Pred. No. 0.00012;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGCG 17
    |||||:|||||
Db 121 CFGRKMDRIGSMSSSLGCG 137

RESULT 20
ANFC ACITR
ID ANFC ACITR STANDARD; PRT; 150 AA.
AC Q76KW6;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide precursor.
GN Name=CNP;
OS Acipenser transmontanus (White sturgeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
OC Acipenser.
OX NCBI_TaxID=7904;
RN [1]
```

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RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
RX PubMed:15072558; DOI=10.1677/jme.0.0320547;
RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
RT sturgeon: identification of BNP in fish lineage.";
RL J. Mol. Endocrinol. 32:547-555(2004).
CC -!- FUNCTION: Vaso relaxant activity. Has a cGMP-stimulating activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in brain, but not in atrium or
CC ventricle.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB087731; BAD02838.1; -; mRNA.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL. 1 31 Potential.
FT PROPEP 32 125 By similarity.
FT PEPTIDE 128 150 C-type natriuretic peptide.
FT DISULFID 134 150 By similarity.
SQ SEQUENCE 150 AA; 15990 MW; D39D9682C35FEC94 CRC64;

Query Match      80.4%; Score 74; DB 1; Length 150;
Best Local Similarity 76.5%; Pred. No. 0.00012;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGCG 17
    |||||:|||||
Db 134 CFGRKMDRIGSMSSSLGCG 150

RESULT 21
Q7YZU5 EPTBU
ID Q7YZU5 EPTBU PRELIMINARY; PRT; 162 AA.
AC Q7YZU5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Natriuretic peptide.
GN Name=NP;
OS Eptatretus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Eptatretinae; Eptatretus.
OX NCBI_TaxID=7764;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kawakoshi A., Hyodo S., Takei Y.;
RL "Hagfish natriuretic peptide precursor mRNA of Eptatretus burgeri.";
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB087732; BAC78816.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological process; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002407; At_natriureticpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; ANATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
KW Vasoactive.
FT CHAIN 94 161 natriuretic peptide.
FT
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SQ SEQUENCE 162 AA; 18220 MW; F4E866403F1A48F7 CRC64;
Query Match 80.4%; Score 74; DB 2; Length 162;
Best Local Similarity 76.5%; Pred. No. 0.00013;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
DB 136 CFGVKMDRIGASTGLGC 152

RESULT 22
Q4SND6_TETNG
ID Q4SND6_TETNG PRELIMINARY; PRT; 25 AA.
AC Q4SND6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 8 SCAF14543, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00015340001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costat C., Bernot A.,
RA Nicaut S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bionet C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie P., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winker P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01014543; CAF97846.1; -; Genomic_DNA.
DR InterPro; IPR002408; Br_natriurtcpep.
DR PRINTS; PR00712; NATPEPTIDES.
DR PRODom; PD005617; NAT_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2727 MW; 8D77FED313F74A90 CRC64;

Query Match 79.3%; Score 73; DB 2; Length 25;
Best Local Similarity 76.5%; Pred. No. 2.8e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
DB 9 CFGKLDRIGSMSGLGC 25

us-10-737-290-172.rup

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RESULT 23
Q9QZ96_CAVPO
ID Q9QZ96_CAVPO PRELIMINARY; PRT; 33 AA.
AC Q9QZ96;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-type natriuretic peptide/factor (Fragment).
GN Name=CNP;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=Hartley; TISSUE=Heart;
RA Aquan K., Thompson L., Weiner C.P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193572; AAF04122.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriurtcpep.
DR InterPro; IPR002406; C_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF0212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR PRODom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT CHAIN <1 33 C-type natriuretic peptide/factor active
FT NON_TER 1 1
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3445 MW; C4DE805DF7E762AE CRC64;

Query Match 79.3%; Score 73; DB 2; Length 33;
Best Local Similarity 76.5%; Pred. No. 3.7e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
DB 17 CFGKLDRIGSMSGLGC 33

RESULT 24
ANFC1_FUGRU
ID ANFC1_FUGRU STANDARD; PRT; 126 AA.
AC Q803D6;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-1 precursor.
GN Name=cnp-1;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=12893874; DOI=10.1073/pnas.1632368100;
RA Inoue K., Naruse K., Yamagami S., Mitani H., Suzuki N., Takei Y.;
RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -!- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
CC CGMP-stimulating activity. May help to regulate body fluid

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CC homeostasis in a variety of aquatic environments.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB089935; BAC57071.1; -; mRNA.
DR Ensemble; SINFUG00000146920; Fugu rubripes.
DR InterPro; IPR002406; C.natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR Hormone; Signal; Vasoactive.
DR FT SIGNAL 1 22 Potential.
DR FT PROPEP 23 102 By similarity.
DR FT PEPTIDE 105 126 C-type natriuretic peptide-1.
DR FT DISULFID 110 126 By similarity.
DR SEQUENCE 126 AA; 14068 MW; DF3F235C2C8D4PF6 CRC64;
CC -----
CC Query Match 79.3%; Score 73; DB 1; Length 126;
CC Best Local Similarity 76.5%; Pred. No. 0.00015;
CC Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
CC -----
QY 1 CFGRKMDRISSSSGLGC 17
DB 110 CFGLKLDRIGSMGLGC 126
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||

RESULT 25
ANFC BOVIN
ID _ANFC BOVIN STANDARD; PRT; 126 AA.
AC PS5206;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB C-type natriuretic peptide precursor (SVSP15) [Contains: CNP-22; CNP-
DE 29; CNP-53].
DE Name=NPPC;
GN Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
OR [1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=94280621; PubMed=8011167;
RX Hosang K.K., Scheit K.K.;
RA "cDNA cloning identified a calmodulin-binding protein in bovine
RT seminal plasma as bovine C-type natriuretic peptide.";
RL DNA Cell Biol. 13:409-417(1994).
CC -1- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Z48478; CAA88369.1; -; mRNA.
DR EMBL; Z48477; CAA88368.1; -; mRNA.
DR InterPro; IPR002406; C.natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.

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RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RP PROTEIN SEQUENCE OF 98-126.
 RX MEDLINE=93112033; PubMed=1472040;
 RA Ishizaka Y., Kangawa K., Minamino N., Ishii K., Takano S., Eto T.,
 RA Matsuo H.;
 RT "Isolation and identification of C-type natriuretic peptide in human
 RT monocytic cell line, THP-1.";
 RL Biochem. Biophys. Res. Commun. 189:697-704(1992).
 CC !- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC !- SIMILARITY: Belongs to the natriuretic peptide family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; M64710; AAA35703.1; -; Genomic DNA.
 CC EMBL; D90337; BAA14351.1; -; Genomic DNA.
 CC EMBL; BC069120; AAH69120.1; -; mRNA.
 CC PIR; JT0567; AWHUC.
 CC FDB; IJDP; X-ray; H=105-126.
 CC Ensembl; ENSG00000163273; Homo sapiens.
 CC HGNC; HGNC:7941; NPCC.
 CC MIM; 600296; -;
 CC GO; GO:0005576; C:extracellular region; NAS.
 CC GO; GO:0008217; P:regulation of blood pressure; NAS.
 CC GO; GO:0019229; P:regulation of vasoconstriction; NAS.
 CC InterPro; IPR002406; C_natriureticpep.
 CC InterPro; IPR000663; Natr_peptide.
 CC Pfam; PF00212; ANP; 1.
 CC PRINTS; PR00713; CNATPEPTIDE.
 CC PRINTS; PR00710; NATPEPTIDES.
 CC ProDom; PD005617; Natr_peptide; 1.
 CC SMART; SM00183; NAT_PEP; 1.
 CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 CC 3D-structure; Direct protein sequencing; Hormone; Polymorphism;
 KW Signal; Vasoactive.
 KW SIGNAL 1 23 Potential.
 FT PROPEP 24 72
 FT PEPTIDE 74 126 CNP-53.
 FT PEPTIDE 98 126 CNP-29.
 FT PEPTIDE 105 126 CNP-22.
 FT DISULFID 110 126 By similarity.
 FT VARIANT 82 82 R -> Q (in dbSNP:5267).
 FT
 FT SEQUENCE 126 AA; 13246 MW; 58F6E657868F9A2D CRC64;
 SQ
 Query Match 79.3%; Score 73; DB 1; Length 126;
 Best Local Similarity 76.5%; Pred. No. 0.00015;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 DB 110 CFGLKLDRIGSMGLGC 126
 |||||:|||||
 RESULT 27
 ANFC MOUSE
 ID ANFC MOUSE STANDARD; PRT; 126 AA.
 AC Q61839;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE C-type natriuretic peptide precursor [Contains: CNP-22; CNP-29; CNP-
 DE 53].
 GN Name=Nppc; Synonyms=Cnp;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX STRAIN=BALB/c;
 RX MEDLINE=95213034; PubMed=7698765;
 RA Ogawa Y., Itoh H., Yoshitake Y., Inoue M., Yoshimasa T., Serikawa T.,
 RA Nakao K.;
 RT "Molecular cloning and chromosomal assignment of the mouse C-type
 RT natriuretic peptide (CNP) gene (Nppc): comparison with the human CNP
 RT gene (NPPC).";
 RL Genomics 24:383-387(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX STRAIN=129/SV;
 RX MEDLINE=97053441; PubMed=8897953;
 RA Huang H., Acuff C.G., Steinhilber M.E.;
 RT "Isolation, mapping, and regulated expression of the gene encoding
 RT mouse C-type natriuretic peptide.";
 RL Am. J. Physiol. 271:H1565-H1575(1996).
 CC !- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC !- SIMILARITY: Belongs to the natriuretic peptide family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; D28873; BAA06028.1; -; Genomic DNA.
 CC EMBL; U62939; AAB61717.1; -; Genomic DNA.
 CC PIR; A55688; A55688.
 CC Ensembl; ENSMUSG00000026241; Mus musculus.
 CC MGI; MGI:97369; Nppc.
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0005184; F:neuropeptide hormone activity; TAS.
 CC GO; GO:0005102; F:receptor binding; IDA.
 CC GO; GO:0006182; P:cGMP biosynthesis; IDA.
 CC InterPro; IPR002406; C_natriureticpep.
 CC InterPro; IPR000663; Natr_peptide.
 CC Pfam; PF00212; ANP; 1.
 CC PRINTS; PR00713; CNATPEPTIDE.
 CC PRINTS; PR00710; NATPEPTIDES.
 CC ProDom; PD005617; Natr_peptide; 1.
 CC SMART; SM00183; NAT_PEP; 1.
 CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Hormone; Signal; Vasoactive.
 KW SIGNAL 1 23 Potential.
 FT PROPEP 24 72
 FT PEPTIDE 74 126 CNP-53 (By similarity).
 FT PEPTIDE 98 126 CNP-29 (By similarity).
 FT PEPTIDE 105 126 CNP-22.
 FT DISULFID 110 126 By similarity.
 FT SEQUENCE 126 AA; 13320 MW; 8F65B1C4B82FOACB CRC64;
 SQ
 Query Match 79.3%; Score 73; DB 1; Length 126;
 Best Local Similarity 76.5%; Pred. No. 0.00015;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 DB 110 CFGLKLDRIGSMGLGC 126
 |||||:|||||
 RESULT 28.
 ANFC FIG
 ID ANFC FIG STANDARD; PRT; 126 AA.
 AC P18104; P21806;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

C-type natriuretic peptide precursor [Contains: CNP-22; CNP-29; CNP-53].
Name=NPPC; Synonyms=CNP;
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
NCBI_TaxID=9823;
[1]
NUCLEOTIDE SEQUENCE.
MEDLINE=91054475; PubMed=2146957;
Tawaragi Y., Fuchimura K., Nakazato H., Tanaka S., Minamino N.,
Kangawa K., Matsuo H.;
"Gene and precursor structure of porcine C-type natriuretic peptide.";
Biochem. Biophys. Res. Commun. 172:627-632(1990).
[2]
PROTEIN SEQUENCE OF 74-126.
TISSUE=Brain;
MEDLINE=90343827; PubMed=2383278;
Minamino N., Kangawa K., Matsuo H.;
"N-terminally extended form of C-type natriuretic peptide (CNP-53)
identified in porcine brain.";
Biochem. Biophys. Res. Commun. 170:973-979(1990).
[3]
PROTEIN SEQUENCE OF 105-126.
TISSUE=Brain;
MEDLINE=90241265; PubMed=2139780;
Sudo T., Minamino N., Kangawa K., Matsuo H.;
"C-type natriuretic peptide (CNP): a new member of natriuretic peptide
family identified in porcine brain.";
Biochem. Biophys. Res. Commun. 168:863-870(1990).
CC -!- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC
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use as long as its content is in no way modified and this statement is not
removed.
EMBL; M64758; AAA31018.1; -; Genomic_DNA.
FIR; A36155; A36155.
DR InterPro; IPR002406; C_natriurtocpep.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Signal; Vasoactive.
FT SIGNAL 1 23 Potential.
FT PROPEP 24 72
FT PEPTIDE 74 126 CNP-53.
FT PEPTIDE 98 126 CNP-29. (By similarity).
FT PEPTIDE 105 126 CNP-22.
FT DISULFID 110 126
SQ SEQUENCE 126 AA; E2474B2D4AABF4DD CRC64;
Query Match 79.3%; Score 73; DB 1; Length 126;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSLGLC 17
DB 110 CFGLKLDRIKMSGLGC 126
RESULT 29
ANFC RAT
ID _ANFC RAT STANDARD; PRT; 126 AA.
AC P55207;

01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
C-type natriuretic peptide precursor [Contains: CNP-22; CNP-29; CNP-53].
Name=NPPC; Synonyms=Cnp;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Murioidea; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
NUCLEOTIDE SEQUENCE.
MEDLINE=91092420; PubMed=1702395; DOI=10.1016/0014-5793(90)80544-S;
Kojima M., Minamino N., Kangawa K., Matsuo H.;
"Cloning and sequence analysis of a cDNA encoding a precursor for rat
C-type natriuretic peptide (CNP).";
FEBS Lett. 276:209-213(1990).
CC -!- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed exclusively in brain.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC
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use as long as its content is in no way modified and this statement is not
removed.
EMBL; D90219; BAA14250.1; -; mRNA.
FIR; S12988; S12988.
DR Ensembl; ENSRNOG0000018854; Rattus norvegicus.
DR RGD; 620850; Nppc.
DR InterPro; IPR002406; C_natriurtocpep.
DR InterPro; IPR006663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 23 Potential.
FT PROPEP 24 72
FT PEPTIDE 74 126 CNP-53.
FT PEPTIDE 98 126 CNP-29. (By similarity).
FT PEPTIDE 105 126 CNP-22.
FT DISULFID 110 126 By similarity.
SQ SEQUENCE 126 AA; 13314 MW; 0957A0DB5B82E08 CRC64;
Query Match 79.3%; Score 73; DB 1; Length 126;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSLGLC 17
DB 110 CFGLKLDRIKMSGLGC 126
RESULT 30
ANFC SHEEP
ID _ANFC SHEEP STANDARD; PRT; 126 AA.
AC P56283;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
C-type natriuretic peptide precursor [Contains: CNP-22; CNP-29; CNP-53].
Name=NPPC; Synonyms=CNP;
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
OC


```

OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99236261; PubMed=10219521; DOI=10.1016/S0739-7240(99)00005-3;
RA Aitken G.D., Raizis A.M., Yandle T.G., George P.M., Espiner E.A.,
RA Cameron V.A.;
RT "The characterization of ovine genes for atrial, brain, and C-type
RT natriuretic peptides.";
RL Domest. Anim. Endocrinol. 16:115-121(1999).
CC -!- FUNCTION: Vaso-relaxant activity. Has a cAMP-stimulating activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF037467; AAB92261.1; -; Genomic_DNA.
DR InterPro; IPR002406; C_natriurtcpep.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 23 Potential.
FT PROPEP 24 72 Potential.
FT PEPTIDE 74 126 CNP-53 (By similarity).
FT PEPTIDE 98 126 CNP-29 (By similarity).
FT PEPTIDE 105 126 CNP-22.
FT DISULFID 110 126 By similarity.
SQ SEQUENCE 126 AA; 13317 MW; 83C21B3C49A8F18B CRC64;

Query Match 79.3%; Score 73; DB 1; Length 126;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CFCRKMDRISSSSGLGC 17
DB 110 CFCGLKLDRIKSGMSGLGC 126

RESULT 31
O4ZG41 HUMAN
AC O4ZG41;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein NPFC.
GN Name=NPFC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kozlowicz A., Spalding L., Tomlinson C.;
RT "The sequence of Homo sapiens BAC clone RP11-52C8.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

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RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC013435; AAX89912.1; -; Genomic_DNA.
DR InterPro; IPR002406; C_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hypothetical protein; Vasoactive.
SQ SEQUENCE 126 AA; 13246 MW; 58F6E657868F9A2D CRC64;

Query Match 79.3%; Score 73; DB 2; Length 126;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CFCRKMDRISSSSGLGC 17
DB 110 CFCGLKLDRIKSGMSGLGC 126

RESULT 32
Q544K5 MOUSE
ID Q544K5 MOUSE PRELIMINARY; PRT; 126 AA.
AC Q544K5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 16 days neonate cerebellum cDNA, RIKEN full-length enriched library,
DE clone:9630044D15 product:natriuretic peptide type C, full insert
DE sequence.
GN Name=NPFC;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyndon P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum; DOI=10.1038/nature01266;
RX MEDLINE=22354683; PubMed=12466851; Adachi J., Bono H., Kondo S.,
RA Okazaki Y., Furuno M., Kasukawa T., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaide I., Oato N., Saito R., Nogaki H., Schonbach C., Gojobori T.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Veraldo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX ADACHI J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Takagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK036176; BAC29333.1; -; mRNA.
DR MGI: MGI.97369; Npcc
DR GO: GO:0005615; C:extracellular space; TAS.
DR
DR GO: GO:0005184; F:neuropeptide hormone activity; TAS.
DR GO: GO:0005102; F:receptor binding; IDA.
DR GO: GO:0006182; P:GMP biosynthesis; IDA.
KW Vasoactive.
SQ SEQUENCE 126 AA; 13320 MW; 8F65B1C4E82F0ACB CRC64;
Query Match 79.3%; Score 73; DB 2; Length 126;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 110 CFGLKLDRISSMSGLGC 126
RESULT 33
ANFCL ONCMY STANDARD; PRT; 131 AA.
AC Q8AXR3;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide I precursor (CNP-22 I).
GN Name=cnp-1;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
ON NCBI_TaxID=8022;
RX Pubmed=12568796; DOI=10.1016/S0016-6480(02)00591-9;
RT "C-type natriuretic peptide of rainbow trout (Oncorhynchus mykiss):
RT primary structure and vasorelaxant activities.";
RL Gen. Comp. Endocrinol. 130:185-192 (2003).
CC -!- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has a
CC GMP-stimulating activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in brain and to a low extent in
CC atrium.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL: AB076603; BAC44842.1; -; mRNA.
DR InterPro: IPR002406; C_natriurtcpep.
DR InterPro: IPR000663; Natri_peptide.
DR Pfam: PF00212; ANP; 1.
DR PRINTS: PR00713; CNATPEPTIDE.
DR PRINTS: PR00710; NATPEPTIDES.
DR ProDom: PD005617; Natri_peptide; 1.
DR SMART: SM00183; NAT_PEP; 1.
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 107 By similarity.
FT PEPTIDE 110 131 C-type natriuretic peptide I.
FT DISULFID 115 131 By similarity.
SQ SEQUENCE 131 AA; 14462 MW; 3A98A2CB78A4F1C3 CRC64;
Query Match 79.3%; Score 73; DB 1; Length 131;
Best Local Similarity 76.5%; Pred. No. 0.00016;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 115 CFGLKLDRISSMSGLGC 131

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Teleostei; Salmoniformes; Salmonidae; Oncorhynchus.
RN NCBI_TaxID=8022;
[1]
RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
RX TISSUE=Brain;
RX PubMed=12586796; DOI=10.1016/S0016-6480(02)00591-9;
RA Inoue K., Russell M.J., Olson K.R., Takei Y.;
RT "C-type natriuretic peptide of rainbow trout (Oncorhynchus mykiss):
RT primary structure and vasorelaxant activities.";
RL Gen. Comp. Endocrinol. 130:185-192(2003)
CC -!- FUNCTION: Exhibits natriuretic and vasodepressor activity. Has a
CC CGMP-stimulating activity (by similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in brain and to a low extent in
CC atrium.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AB076602; BAC44843.1; -; mRNA.
DR InterPro; IPR002406; C_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 107 By similarity.
FT PEPTIDE 110 131 C-type natriuretic peptide II.
FT DISULFID 115 131 By similarity.
SQ SEQUENCE 131 AA; 14472 MW; 436CF382B326A08D CRC64;

Query Match 79.3%; Score 73; DB 1; Length 131;
Best Local Similarity 76.5%; Pred. No. 0.00016;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKWDRISSSSGLGC 17
Db 115 CFGLKLDRIGMSGLGC 131

RESULT 36
Q805E7 OREMO
ID Q805E7 OREMO PRELIMINARY; PRT; 131 AA.
AC Q805E7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-type natriuretic peptide.
GN Name=cnp;
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; African cichlids; Pseudocrenilabrinae; Tilapiini;
OC Oreochromis.
OX NCBI_TaxID=8127;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Inoue K., Takei Y.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB008728; BAC55026.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.

```

DR GO; GO:0005179; F: hormone activity; IEA.
 DR GO; GO:0050880; P: regulation of blood vessel size; IEA.
 DR InterPro; IPR002408; Br_natriurtcpep.
 DR InterPro; IPR002406; C_natriurtcpep.
 DR InterPro; IPR000663; Natr_peptide.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00712; BNATPEPTIDE.
 DR PRINTS; PR00713; CNATPEPTIDES.
 DR PRINTS; PR00710; NATPEPTIDES.
 DR ProDom; PD005617; Natr_peptide; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Vasoactive.
 SQ SEQUENCE 131 AA; 14601 MW; F9DCBBE28CC0E7C CRC64;

Query Match 79.3%; Score 73; DB 2; Length 131;
 Best Local Similarity 76.5%; Pred. No. 0.00016;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSLGIC 17
 |||:|||||
 Db 115 CFCGLKLDRIKSGMSGLIC 131

RESULT 37

Q5Y820_XENLA PRELIMINARY; PRT; 137 AA.
 AC Q5Y820;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Natriuretic peptide type B.
 GN Name=Nppb;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15736168; DOI=10.1002/dvdy.20274;
 RA Smith S.J., Ataliotis P., Kotecha S., Towers N., Sparrow D.B.,
 RA Mohun T.J.;
 RT "The MLCiv gene provides a transgenic marker of myocardium formation
 within developing chambers of the Xenopus heart.";
 RL Dev. Dyn. 232:1003-1012(2005).
 DR EMBL; AY660659; AAU88199.1; -; mRNA.
 DR GO; GO:0005576; C: extracellular region; IEA.
 DR GO; GO:0005179; F: hormone activity; IEA.
 DR GO; GO:0050880; P: regulation of blood vessel size; IEA.
 DR InterPro; IPR002408; Br_natriurtcpep.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00712; BNATPEPTIDE.
 DR PRINTS; PR00710; NATPEPTIDES.
 DR ProDom; PD005617; Natr_peptide; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Vasoactive.
 SQ SEQUENCE 137 AA; 15380 MW; 0F7394ACCCBB99EA CRC64;

Query Match 79.3%; Score 73; DB 2; Length 137;
 Best Local Similarity 70.6%; Pred. No. 0.00016;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSLGIC 17
 |||:|||||
 Db 115 CFCRRIDRISLSGMIC 131

RESULT 38

Q4T953_TETNG PRELIMINARY; PRT; 138 AA.
 ID Q4T953_TETNG

AC Q4T953;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAF7638, whole genome shotgun sequence.
 DE (Fragment).
 DE ORFNames=GSTENG0004914001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; CA901007638; CAF90579.1; -; Genomic_DNA.
 DR InterPro; IPR002408; Br_natriurtcpep.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00712; BNATPEPTIDE.
 DR PRINTS; PR00710; NATPEPTIDES.
 DR ProDom; PD005617; Natr_peptide; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Vasoactive.
 FT NON_TER 138 138
 SQ SEQUENCE 138 AA; 15212 MW; E244D7D6F9BE3BF4 CRC64;

Query Match 79.3%; Score 73; DB 2; Length 138;
 Best Local Similarity 70.6%; Pred. No. 0.00017;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSLGIC 17
 |||:|||||
 Db 117 CFCGRMDRIGNASGLIC 133

RESULT 39

ANF_FUGRU STANDARD; PRT; 139 AA.
 ID ANF_FUGRU

AC Q805D8;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
 DE (ANP) (Prepronatriodilatin).
 DE Name=ANP;
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

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OC Tetradontidae; Tetradontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA PubMed=15072558; DOI=10.1677/jme.0.0320547;
RX Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
RT sturgeon: identification of BNP in fish lineage.";
RL J. Mol. Endocrinol. 32:547-555(2004).
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AB089933; BAC57069.1; -; mRNA.
DR InterPro; IPR002407; At_natriurtcpep.
DR Ensembl; ENSGALG00000004574; Natr_peptide.
DR PANTHER; PTHR11415; At_natriurtcpep; 1.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 21 Potential.
FT PROPEP 22 112
FT PEPTIDE 115 139 Atrial natriuretic factor.
FT DISULFID 118 134 By similarity.
SQ SEQUENCE 139 AA; 15569 MW; EC9CBE9D5C31220 CRC64;

Query Match 79.3%; Score 73; DB 1; Length 139;
Best Local Similarity 70.6%; Pred. No. 0.00017;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGCG 17
DB 118 CFGRMDRIGNASGLGC 134
|||:||||:|||||
ANF_OREMO STANDARD; PRT; 140 AA.

RESULT 40
ANF_CHICK
ID ANF_CHICK STANDARD; PRT; 140 AA.
AC P18908;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
DE (ANP) (prepronatriodilatin).
GN Name=NPPA;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91192169; PubMed=1826483; DOI=10.1016/0014-5793(91)80331-V;
RA Akizuki N., Kangawa K., Minamino N., Matsuo H.;
RT "Cloning and sequence analysis of complementary DNA encoding a
RT precursor for chicken natriuretic peptide.";
RL FEBS Lett. 280:357-362(1991).
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X57702; CAA40879.1; -; mRNA.
DR PIR; S14320; S14320.
DR Ensembl; ENSGALG00000004574; Gallus gallus.
DR InterPro; IPR002408; Br_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Signal; Vasoactive.
FT SIGNAL 1 24 Potential.
FT PROPEP 25 110 Atrial natriuretic factor.
FT PEPTIDE 112 140
FT DISULFID 118 134
SQ SEQUENCE 140 AA; 15714 MW; 67FEBFE094E71F40 CRC64;

Query Match 79.3%; Score 73; DB 1; Length 140;
Best Local Similarity 70.6%; Pred. No. 0.00017;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGCG 17
DB 118 CFGRMDRIGNASGLGC 134
|||:||||:|||||
ANF_OREMO STANDARD; PRT; 140 AA.

RESULT 41
ANF_OREMO
ID ANF_OREMO STANDARD; PRT; 140 AA.
AC Q805E9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Atrial natriuretic factor precursor (ANP) (Atrial natriuretic peptide)
DE (ANP) (prepronatriodilatin).
GN Name=ANP;
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; African cichlids; Pseudocrenilabrinae; Tilapiini;
OC Oreochromis.
OX NCBI_TaxID=8127;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
RT sturgeon: identification of BNP in fish lineage.";
RL J. Mol. Endocrinol. 32:547-555(2004).
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC

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RA Miyata A., Minamino N., Kangawa K., Matsuo H.;
RT "Identification of a 29-amino acid natriuretic peptide in chicken
RT heart.";
RL Biochem. Biophys. Res. Commun. 155:1330-1337(1988).
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X57702; CAA40879.1; -; mRNA.
DR PIR; S14320; S14320.
DR Ensembl; ENSGALG00000004574; Gallus gallus.
DR InterPro; IPR002408; Br_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Signal; Vasoactive.
FT SIGNAL 1 24 Potential.
FT PROPEP 25 110 Atrial natriuretic factor.
FT PEPTIDE 112 140
FT DISULFID 118 134
SQ SEQUENCE 140 AA; 15714 MW; 67FEBFE094E71F40 CRC64;

Query Match 79.3%; Score 73; DB 1; Length 140;
Best Local Similarity 70.6%; Pred. No. 0.00017;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGCG 17
DB 118 CFGRMDRIGNASGLGC 134
|||:||||:|||||
ANF_OREMO STANDARD; PRT; 140 AA.

RESULT 41
ANF_OREMO
ID ANF_OREMO STANDARD; PRT; 140 AA.
AC Q805E9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Atrial natriuretic factor precursor (ANP) (Atrial natriuretic peptide)
DE (ANP) (prepronatriodilatin).
GN Name=ANP;
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; African cichlids; Pseudocrenilabrinae; Tilapiini;
OC Oreochromis.
OX NCBI_TaxID=8127;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
RT sturgeon: identification of BNP in fish lineage.";
RL J. Mol. Endocrinol. 32:547-555(2004).
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB087283; BAC55024.1; -; mRNA.
DR InterPro; IPR002407; At_natriurtcpep.
DR PANTHER; PTHR11415; At_natriurtcpep; 1.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; NATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_Peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive. Potential.
FT SIGNAL 1 21
FT PROPEP 22 113
FT PEPTIDE 116 140 Atrial natriuretic factor.
FT DISULFID 119 135 By similarity.
SQ SEQUENCE 140 AA; 15577 MW; 5F2D214FA560DB0F CRC64;

Query Match 79.3%; Score 73; DB 1; Length 140;
Best Local Similarity 70.6%; Pred. No. 0.00017;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   |||:||||:|||||
DB 119 CFGRKMDRIGNASGLGC 135

RESULT 42
Q8VHG9 NOTAL PRELIMINARY; PRT; 147 AA.
AC Q8VHG9;
DT 01-WAR-2002 (TREMBLrel. 20, Created)
DT 01-WAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE C-type natriuretic peptide hormone.
OS Notoxys alexis (Spinifex hopping mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Notomys.
OX NCBI_TaxID=184396;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22978641; PubMed=14613785; DOI=10.1016/S1095-6433(03)00207-1;
RA Heimeier R.A., Donald J.A.;
RT "Renal C-type natriuretic peptide and natriuretic peptide receptor B
RT mRNA expression are affected by water deprivation in the Spinifex
RT Hopping mouse.";
RL Comp. Biochem. Physiol., Part A Mol. Integr. Physiol.
RL 136:565-575(2003).
DR EMBL; AF460241; AAL6744.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriurtcpep.
DR InterPro; IPR002406; C_natriurtcpep.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_Peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPPTIDE; 1.
KW Vasoactive.

SQ SEQUENCE 147 AA; 15321 MW; 66F916DB9A853238 CRC64;

Query Match 79.3%; Score 73; DB 2; Length 147;
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Best Local Similarity 76.5%; Pred. No. 0.00018;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   |||:||||:|||||
DB 131 CFGLKLDRIKMSGLGC 147

RESULT 43
Q90Y11 CRODU PRELIMINARY; PRT; 181 AA.
AC Q90Y11;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE Bradykinin potentiating peptide and C-type natriuretic peptide isoform
DE 2.
OS Crotalus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8732;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Venom gland;
RA Hayashi M.A.F., Radis-Baptista G., Barbosa S.R., Yamane T.,
RA Camargo A.C.M.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF308594; AAL09427.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 181 AA; 18507 MW; 9B2E95D38AA5FF27 CRC64;

Query Match 79.3%; Score 73; DB 2; Length 181;
Best Local Similarity 76.5%; Pred. No. 0.00022;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   |||:||||:|||||
DB 165 CFGLKLDRIKMSGLGC 181

RESULT 44
Q90Y12 CRODU PRELIMINARY; PRT; 181 AA.
AC Q90Y12;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE Bradykinin potentiating peptide and C-type natriuretic peptide isoform
DE 1.
OS Crotalus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8732;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Venom gland;
RA Hayashi M.A.F., Radis-Baptista G., Barbosa S.R., Yamane T.,
RA Camargo A.C.M.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF308593; AAL09426.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
```

DR GO: GO:0050880; P:regulation of blood vessel size; IEA.
 DR InterPro: IPR000663; Natr_peptide.
 DR Pfam: PF00212; ANP; 1.

DR PRINTS: PR00710; NATPEPTIDES.
 DR ProDom: PD005617; Natr_peptide; 1.

DR SMART: SM00183; NAT_PEP; 1.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.

KW Vasoactive.
 SQ SEQUENCE 181 AA; 18560 MW; 7BSADCSB9372D07F CRC64;

Query Match 79.3%; Score 73; DB 2; Length 181;
 Best Local Similarity 76.5%; Pred. No. 0.00022;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGQC 17
 |||||:|||||
 DB 165 CFGLKLDRIKSGSLGQC 181

RESULT 45

ID ANFC_CHICK STANDARD; PRT; 22 AA.
 AC P21805; (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C-type natriuretic peptide (CNP).

OS Names=NPPC;
 GN Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;

OC Gallus.
 OC NCBI_TaxID=9031;

QY 1
 RN [1]

RP TISSUE=Brain;
 RC MEDLINE=91113186; PubMed=1989595;

RX Arimura J.J., Minamino N., Kangawa K., Matsuo H.;
 RA "Isolation and identification of C-type natriuretic peptide in chicken

RT brain."
 RL Biochem. Biophys. Res. Commun. 174:142-148(1991).

CC -!- FUNCTION: Vasoactive activity. Has a cGMP-stimulating activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC PIR: JTO581; JTO581.
 DR Ensembl: ENSGALG00000004572; Gallus gallus.

DR InterPro: IPR002408; Br_natriurtcpep.
 DR InterPro: IPR000663; Natr_peptide.

DR Pfam: PF00212; ANP; 1.
 DR PRINTS: PR00712; NATPEPTIDES.

DR PRINTS: PR00710; NATPEPTIDES.
 DR ProDom: PD005617; Natr_peptide; 1.

DR SMART: SM00183; NAT_PEP; 1.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.

KW Direct protein sequencing; Hormone; Vasoactive.
 FT DISULFID 6 22

SQ SEQUENCE 22 AA; 2244 MW; FC2A4706D8DAC025 CRC64;

Query Match 78.3%; Score 72; DB 1; Length 22;
 Best Local Similarity 76.5%; Pred. No. 3.7e-05;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGQC 17
 |||||:|||||
 DB 6 CFGLKLDRIKSGSLGQC 22

RESULT 46

ANF ANGJA STANDARD; PRT; 27 AA.
 ID ANF ANGJA

AC P18144;
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Atrial natriuretic factor (ANF) (Atrial natriuretic peptide) (ANP).
 OS Anguilla japonica (Japanese eel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;

OC Anguilla.
 OC NCBI_TaxID=7937;

RN [1]
 RP PROTEIN SEQUENCE.

RC TISSUE=Heart atrium;
 RX MEDLINE=90026430; PubMed=2529857;

RA Takei Y., Takahashi A., Watanabe T.X., Nakajima K., Sakakibara S.;
 RT "Amino acid sequence and relative biological activity of eel atrial

RT natriuretic peptide."
 RL Biochem. Biophys. Res. Commun. 164:537-543(1989).

CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
 CC key role in cardiovascular homeostasis. Has a cGMP-stimulating

CC activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC PIR: A33431; A33431.
 DR InterPro: IPR002407; At_natriurtcpep.

DR InterPro: IPR002408; Br_natriurtcpep.
 DR InterPro: IPR000663; Natr_peptide.

DR PANTHER: PTHR11415; At_natriurtcpep; 1.
 DR Pfam: PF00212; ANP; 1.

DR PRINTS: PR00712; BNATPEPTIDE.
 DR PRINTS: PR00710; NATPEPTIDES.

DR ProDom: PD005107; At_natriurtcpep; 1.
 DR ProDom: PD005617; Natr_peptide; 2.

DR SMART: SM00183; NAT_PEP; 1.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.

KW Direct protein sequencing; Hormone; Vasoactive.
 FT DISULFID 7 23

SQ SEQUENCE 27 AA; 2792 MW; 9EF5100CCF282B4D CRC64;

Query Match 78.3%; Score 72; DB 1; Length 27;
 Best Local Similarity 76.5%; Pred. No. 4.5e-05;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGQC 17
 |||||:|||||

DB 7 CFGLKLDRIKSGSLGQC 23

Query Match 78.3%; Score 72; DB 1; Length 27;
 Best Local Similarity 76.5%; Pred. No. 4.5e-05;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGQC 17
 |||||:|||||

DB 7 CFGLKLDRIKSGSLGQC 23

RESULT 47

Q4S797_TETNG
 ID Q4S797_TETNG PRELIMINARY; PRT; 101 AA.

AC Q4S797;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Chromosome 1 SCAF14716, whole genome shotgun sequence.
 GN ORFNames=GSTENG002208001;

OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

```

CC NCBI_TaxID=99883;
CC [1]
CC NUCLEOTIDE SEQUENCE.
CC RA Jaitillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
CC RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
CC RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
CC RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
CC RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
CC RA Bionnet C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
CC RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
CC RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
CC RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
CC RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
CC RA Laudet V., Schacherer V., Quetier F., Saurin W., Scarpelli C.,
CC RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
CC RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
CC RT the early vertebrate proto-karyotype."
CC RL Nature 431:946-957(2004).
CC [2]
CC NUCLEOTIDE SEQUENCE.
CC RP Genoscope; Whitehead Institute Centre for Genome Research;
CC RP Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC RL -!- CAUTION: The sequence shown here is derived from an
CC CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC CC preliminary data.
CC DR EMBL; CAAB01014716; GAG03485.1; -; Genomic_DNA.
CC DR InterPro; IPR002406; C_natriurtcpep.
CC DR InterPro; IPR000663; Natr_peptide.
CC DR Pfam; PF00212; ANP; 1.
CC DR PRINTS; PR00713; CNATPEPTIDE.
CC DR PRINTS; PR00710; NATPEPTIDES.
CC DR ProDom; PD005617; Natr_peptide; 1.
CC DR SMART; SM00183; NAT_PEP; 1.
CC DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
CC KW Vasoactive.
CC SQ SEQUENCE 101 AA; 11398 MW; 31CA29F92812C3D0 CRC64;

Query Match 78.3%; Score 72; DB 2; Length 101;
Best Local Similarity 70.6%; Pred. No. 0.00018;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFCRKNDRISSSSLGCG 17
DB 85 CFCGKMDRIGTISGMGC 101
||| ||||| : ||: ||

RESULT 48
ANFC4_FUGRU STANDARD; PRT; 120 AA.
AC Q805D3;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-4 precursor.
GN Name=cnp-4;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=12893874; DOI=10.1073/pnas.1632368100;
RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -!- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
CC CGMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC OX NCBI_TaxID=31033;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=12893874; DOI=10.1073/pnas.1632368100;
RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -!- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
CC CGMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC DR EMBL; AB091699; BAC65998.1; -; mRNA.
CC InterPro; IPR002408; Br_natriurtcpep.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.

CC NCBI_TaxID=99883;
CC [1]
CC NUCLEOTIDE SEQUENCE.
CC RA Jaitillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
CC RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
CC RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
CC RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
CC RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
CC RA Bionnet C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
CC RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
CC RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
CC RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
CC RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
CC RA Laudet V., Schacherer V., Quetier F., Saurin W., Scarpelli C.,
CC RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
CC RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
CC RT the early vertebrate proto-karyotype."
CC RL Nature 431:946-957(2004).
CC [2]
CC NUCLEOTIDE SEQUENCE.
CC RP Genoscope; Whitehead Institute Centre for Genome Research;
CC RP Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC RL -!- CAUTION: The sequence shown here is derived from an
CC CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC CC preliminary data.
CC DR EMBL; CAAB01014716; GAG03485.1; -; Genomic_DNA.
CC DR InterPro; IPR002406; C_natriurtcpep.
CC DR InterPro; IPR000663; Natr_peptide.
CC DR Pfam; PF00212; ANP; 1.
CC DR PRINTS; PR00713; CNATPEPTIDE.
CC DR PRINTS; PR00710; NATPEPTIDES.
CC DR ProDom; PD005617; Natr_peptide; 1.
CC DR SMART; SM00183; NAT_PEP; 1.
CC DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
CC KW Vasoactive.
CC SQ SEQUENCE 101 AA; 11398 MW; 31CA29F92812C3D0 CRC64;

Query Match 78.3%; Score 72; DB 1; Length 120;
Best Local Similarity 70.6%; Pred. No. 0.00022;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFCRKNDRISSSSLGCG 17
DB 104 CFCGKMDRIGTISGMGC 120
||| ||||| : ||: ||

RESULT 49
ANFC4_ORYLA STANDARD; PRT; 121 AA.
AC Q800I7;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-4 precursor.
GN Name=cnp-4;
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RN NUCLEOTIDE SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=12893874; DOI=10.1073/pnas.1632368100;
RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -!- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
CC CGMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Brain, spinal cord, spleen, heart and fin, and
CC to a lower extent in gill and ovary.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AB089938; BAC57074.1; -; mRNA.
CC Ensembl; SINFRUG00000151691; Fugu rubripes.
CC InterPro; IPR002406; C_natriurtcpep.
CC InterPro; IPR000663; Natr_peptide.
CC Pfam; PF00212; ANP; 1.
CC PRINTS; PR00713; CNATPEPTIDE.
CC PRINTS; PR00710; NATPEPTIDES.
CC ProDom; PD005617; Natr_peptide; 1.
CC SMART; SM00183; NAT_PEP; 1.
CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
CC KW Hormone; Signal; Vasoactive.
CC FT SIGNAL 1 22 Potential.
CC FT PROPEP 23 94 By similarity.
CC FT PEPTIDE 97 120 C-type natriuretic peptide-4.
CC FT DISULFID 104 120 By similarity.
CC SQ SEQUENCE 120 AA; 13504 MW; 27233AEC1FA3313E CRC64;

Query Match 78.3%; Score 72; DB 1; Length 120;
Best Local Similarity 70.6%; Pred. No. 0.00022;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFCRKNDRISSSSLGCG 17
DB 104 CFCGKMDRIGTISGMGC 120
||| ||||| : ||: ||

RESULT 49
ANFC4_ORYLA STANDARD; PRT; 121 AA.
AC Q800I7;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-4 precursor.
GN Name=cnp-4;
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RN NUCLEOTIDE SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=12893874; DOI=10.1073/pnas.1632368100;
RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -!- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
CC CGMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Brain, spinal cord, spleen, heart and fin, and
CC to a lower extent in gill and ovary.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AB091699; BAC65998.1; -; mRNA.
CC InterPro; IPR002408; Br_natriurtcpep.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.

```



```
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; ENATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 94 By similarity.
FT PEPTIDE 97 121 C-type natriuretic peptide-4.
FT DISULFID 105 121 By similarity.
SQ SEQUENCE 121 AA; 13457 MW; EFD7FD534B137009 CRC64;

Query Match 78.3%; Score 72; DB 1; Length 121;
Best Local Similarity 70.6%; Pred. No. 0.0022;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSGLGC 17
DB 105 CFCGRKMDRIGTISGMGC 121

RESULT 50
ANFC2_FUGRU
ID ANFC2_FUGRU STANDARD; PRT; 130 AA.
AC Q80SD5;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-2 precursor.
GN Name=cnp-2;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_Taxid=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=12893874; DOI=10.1073/pnas.1632368100;
RA Inoue K., Naruse K., Yamagami S., Mitani H., Suzuki N., Takei Y.;
RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -!- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
CC CGMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
-----
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
DR EMBL; AB089936; BAC57072.1; -; mRNA.
DR Ensembl; SINFRUG00000157592; Fugu rubripes.
DR InterPro; IPR002406; C_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 101 By similarity.
FT PEPTIDE 104 130 C-type natriuretic peptide-2.
FT DISULFID 114 130 By similarity.
```

```
SQ SEQUENCE 130 AA; 13792 MW; 41BE1FC1A5F7E4C CRC64;

Query Match 78.3%; Score 72; DB 1; Length 130;
Best Local Similarity 76.5%; Pred. No. 0.00023;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSGLGC 17
DB 114 CFCGRKMDRISSSSGLGC 130

Search completed: January 25, 2006, 18:48:18
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Title: US-10-737-290-172
Perfect score: 92
Sequence: 1 CPGKMDRISSSSGLGC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

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SUMMARIES

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262	67	72.8	21	2	US-09-623-548A-483	Sequence 483, App	335	66	71.7	32	1	US-08-451-240-5	Sequence 5, Appli
263	67	72.8	21	2	US-09-657-276-483	Sequence 483, App	336	66	71.7	32	1	US-08-470-846A-5	Sequence 5, Appli
264	67	72.8	21	6	5212286-41	Patent No. 5212286	337	66	71.7	32	2	US-08-954-915A-27	Sequence 27, Appl
265	67	72.8	22	1	US-08-257-446-1	Sequence 1, Appli	338	66	71.7	32	2	US-09-154-390-5	Sequence 5, Appli
266	67	72.8	22	6	5212286-38	Patent No. 5212286	339	66	71.7	32	6	PCT-US94-12591-5	Patent No. 5212286
267	67	72.8	23	2	US-09-623-548A-484	Sequence 484, App	340	65	70.7	20	6	5212286-58	Patent No. 5212286
268	67	72.8	23	2	US-09-657-276-484	Sequence 484, App	341	65	70.7	24	6	5212286-56	Patent No. 5212286
269	67	72.8	23	6	5212286-29	Patent No. 5212286	342	65	70.7	25	6	5212286-55	Patent No. 5212286
270	67	72.8	23	6	5212286-37	Patent No. 5212286	343	65	70.7	32	2	US-08-954-915A-2	Sequence 2, Appli
271	67	72.8	24	1	US-08-257-446-5	Sequence 5, Appli	344	65	70.7	32	2	US-08-954-915A-3	Sequence 3, Appli
272	67	72.8	24	2	US-09-623-548A-485	Sequence 485, App	345	65	70.7	35	2	US-09-623-548A-506	Sequence 506, App
273	67	72.8	24	2	US-09-623-548A-487	Sequence 487, App	346	65	70.7	35	2	US-09-657-276-506	Sequence 506, App
274	67	72.8	24	2	US-09-623-548A-502	Sequence 502, App	347	65	70.7	45	2	US-08-954-915A-47	Sequence 47, Appl
275	67	72.8	24	2	US-09-623-548A-505	Sequence 505, App	348	65	70.7	45	2	US-09-623-548A-510	Sequence 510, App
276	67	72.8	24	2	US-09-657-276-485	Sequence 485, App	349	65	70.7	45	2	US-09-657-276-510	Sequence 510, App
277	67	72.8	24	2	US-09-657-276-487	Sequence 487, App	350	64	69.6	17	6	5212286-42	Patent No. 5212286
278	67	72.8	24	2	US-09-657-276-502	Sequence 502, App	351	64	69.6	18	6	5212286-42	Patent No. 5212286
279	67	72.8	24	2	US-09-657-276-505	Sequence 505, App	352	64	69.6	21	2	US-09-466-268B-8	Sequence 8, Appli
280	67	72.8	24	6	5212286-26	Patent No. 5212286	353	64	69.6	22	1	US-07-828-450-26	Sequence 26, Appl
281	67	72.8	25	2	US-09-623-548A-488	Sequence 488, App	354	64	69.6	22	1	US-07-828-450-27	Sequence 27, Appl
282	67	72.8	25	2	US-09-657-276-488	Sequence 488, App	355	64	69.6	22	1	US-07-828-450-28	Sequence 28, Appl
283	67	72.8	25	6	5212286-25	Patent No. 5212286	356	64	69.6	22	1	US-07-828-450-29	Sequence 29, Appl
284	67	72.8	25	6	5212286-34	Patent No. 5212286	357	64	69.6	22	1	US-08-297-330-9	Sequence 9, Appli
285	67	72.8	26	1	US-07-781-590A-1	Sequence 1, Appli	358	64	69.6	22	4	PCT-US94-02391-9	Sequence 9, Appli
286	67	72.8	26	2	US-09-623-548A-478	Sequence 478, App	359	64	69.6	32	2	US-08-954-915A-25	Sequence 25, Appl
287	67	72.8	26	2	US-09-657-276-478	Sequence 478, App	360	64	69.6	32	2	US-08-954-915A-28	Sequence 28, Appl
288	67	72.8	28	1	US-07-754-958-3	Sequence 3, Appli	361	63	68.5	23	2	US-10-106-806-11	Sequence 11, Appl
289	67	72.8	28	1	US-07-754-947-3	Sequence 3, Appli	362	63	68.5	32	2	US-09-623-548A-513	Sequence 513, App
290	67	72.8	28	1	US-08-451-240-9	Sequence 9, Appli	363	63	68.5	32	2	US-09-657-276-513	Sequence 513, App
291	67	72.8	28	1	US-08-451-240-25	Sequence 25, Appl	364	63	68.5	38	2	US-09-466-268B-10	Sequence 10, Appl
292	67	72.8	28	1	US-08-240-711-21	Sequence 21, Appl	365	63	68.5	38	2	US-10-106-806-10	Sequence 10, Appl
293	67	72.8	28	1	US-08-457-753-21	Sequence 21, Appl	366	63	68.5	45	2	US-08-954-915A-46	Sequence 46, Appl
294	67	72.8	28	1	US-08-470-846A-9	Sequence 9, Appli	367	63	68.5	45	2	US-09-623-548A-514	Sequence 514, App
295	67	72.8	28	2	US-08-470-846A-27	Sequence 27, Appl	368	63	68.5	45	2	US-09-657-276-514	Sequence 514, App
296	67	72.8	28	2	US-08-954-915A-51	Sequence 51, Appl	369	62	67.4	21	1	US-07-781-590A-15	Sequence 15, Appl
297	67	72.8	28	2	US-09-154-390-9	Sequence 9, Appli	370	62	67.4	28	1	US-08-470-846A-23	Sequence 23, Appl
298	67	72.8	28	2	US-09-154-390-23	Sequence 23, Appl	371	61	66.3	20	6	5212286-54	Patent No. 5212286
299	67	72.8	28	2	US-09-154-390-27	Sequence 27, Appl	372	61	66.3	23	6	5212286-43	Patent No. 5212286
300	67	72.8	28	2	US-09-623-548A-486	Sequence 486, App	373	61	66.3	23	6	5212286-45	Patent No. 5212286
301	67	72.8	28	4	US-09-657-276-486	Sequence 486, App	374	61	66.3	23	6	5212286-53	Patent No. 5212286
302	67	72.8	28	4	PCT-US94-12591-9	Sequence 9, Appli	375	61	66.3	24	6	5212286-52	Patent No. 5212286
303	67	72.8	28	6	PCT-US94-12591-25	Sequence 25, Appl	376	61	66.3	25	6	5212286-31	Patent No. 5212286
304	67	72.8	28	6	5204327-3	Patent No. 5204327	377	61	66.3	25	6	5212286-33	Patent No. 5212286
305	67	72.8	32	2	US-08-954-915A-13	Sequence 13, Appl	378	61	66.3	28	1	US-08-451-240-8	Sequence 8, Appli
306	67	72.8	32	2	US-08-954-915A-29	Sequence 29, Appl	379	61	66.3	28	1	US-08-470-846A-8	Sequence 8, Appli
307	67	72.8	32	2	US-09-623-548A-490	Sequence 490, App	380	61	66.3	28	2	US-09-154-390-8	Sequence 8, Appli
308	67	72.8	32	2	US-09-657-276-490	Sequence 490, App	381	61	66.3	28	4	PCT-US94-12591-8	Sequence 8, Appli
309	67	72.8	152	2	US-08-916-043-2	Sequence 2, Appli	382	60	65.2	23	1	US-07-781-590A-16	Sequence 16, Appl
310	67	72.8	152	2	US-09-428-929-2	Sequence 2, Appli	383	60	65.2	28	1	US-08-451-240-10	Sequence 10, Appl
311	67	72.8	152	6	5212286-6	Patent No. 5212286	384	60	65.2	28	1	US-08-451-240-23	Sequence 23, Appl
312	66	71.7	20	2	US-09-579-883A-13	Sequence 13, Appl	385	60	65.2	28	1	US-08-470-846A-10	Sequence 10, Appl
313	66	71.7	20	2	US-09-623-548A-469	Sequence 469, App	386	60	65.2	28	1	US-08-470-846A-25	Sequence 25, Appl
314	66	71.7	20	2	US-09-657-276-469	Sequence 469, App	387	60	65.2	28	1	US-09-154-390-10	Sequence 10, Appl
315	66	71.7	21	2	US-09-623-548A-470	Sequence 470, App	388	60	65.2	28	2	US-09-154-390-25	Sequence 25, Appl
316	66	71.7	21	2	US-09-657-276-470	Sequence 470, App	389	60	65.2	28	4	PCT-US94-12591-10	Sequence 10, Appl
317	66	71.7	22	1	US-07-828-450-18	Sequence 18, Appl	390	60	65.2	28	4	PCT-US94-12591-23	Sequence 23, Appl
318	66	71.7	23	6	5212286-48	Patent No. 5212286	391	60	65.2	32	2	US-08-954-915A-7	Sequence 7, Appli
319	66	71.7	24	1	US-07-754-958-4	Sequence 4, Appli	392	60	65.2	32	2	US-08-954-915A-8	Sequence 8, Appli

393	59	64.1	20	1	US-08-257-446-4	Sequence 4, Appli	466	48	52.2	22	2	US-09-154-390-32	Sequence 32, Appl
394	59	64.1	28	1	US-08-451-240-24	Sequence 24, Appl	467	48	52.2	22	4	PCT-US94-12591-29	Sequence 29, Appl
395	59	64.1	28	1	US-08-470-846A-26	Sequence 26, Appl	468	48	52.2	22	4	PCT-US94-12591-30	Sequence 30, Appl
396	59	64.1	28	1	US-09-154-390-26	Sequence 26, Appl	469	47	51.1	22	1	US-08-451-240-20	Sequence 20, Appl
397	59	64.1	28	4	PCT-US94-12591-24	Sequence 24, Appl	470	47	51.1	22	1	US-08-470-846A-20	Sequence 20, Appl
398	58	63.0	17	1	US-07-828-450-20	Sequence 20, Appl	471	47	51.1	22	2	US-09-154-390-20	Sequence 20, Appl
399	57	62.0	20	1	US-08-257-446-3	Sequence 3, Appli	472	47	51.1	22	4	PCT-US94-12591-20	Sequence 20, Appl
400	57	62.0	28	1	US-08-470-846A-22	Sequence 22, Appl	473	47	51.1	28	1	US-08-451-240-17	Sequence 17, Appl
401	56	60.9	28	1	US-08-451-240-11	Sequence 11, Appl	474	47	51.1	28	1	US-08-451-240-31	Sequence 31, Appl
402	56	60.9	28	1	US-08-451-240-34	Sequence 34, Appl	475	47	51.1	28	1	US-08-470-846A-17	Sequence 17, Appl
403	56	60.9	28	1	US-08-470-846A-11	Sequence 11, Appl	476	47	51.1	28	2	US-09-154-390-17	Sequence 17, Appl
404	56	60.9	28	1	US-08-470-846A-19	Sequence 19, Appl	477	47	51.1	28	2	US-09-154-390-33	Sequence 33, Appl
405	56	60.9	28	1	US-08-470-846A-31	Sequence 31, Appl	478	47	51.1	28	4	PCT-US94-12591-17	Sequence 17, Appl
406	56	60.9	28	1	US-08-470-846A-32	Sequence 32, Appl	479	47	51.1	28	4	PCT-US94-12591-31	Sequence 31, Appl
407	56	60.9	28	2	US-09-154-390-11	Sequence 11, Appl	480	47	51.1	29	1	US-08-451-240-27	Sequence 27, Appl
408	56	60.9	28	2	US-09-154-390-19	Sequence 19, Appl	481	47	51.1	29	1	US-08-451-240-28	Sequence 28, Appl
409	56	60.9	28	2	US-09-154-390-38	Sequence 38, Appl	482	47	51.1	29	2	US-08-470-846A-29	Sequence 29, Appl
410	56	60.9	28	4	PCT-US94-12591-11	Sequence 11, Appl	483	47	51.1	29	2	US-09-154-390-29	Sequence 29, Appl
411	56	60.9	32	1	US-08-451-240-15	Sequence 15, Appl	484	47	51.1	29	2	US-09-154-390-30	Sequence 30, Appl
412	56	60.9	32	1	US-08-470-846A-15	Sequence 15, Appl	485	47	51.1	29	4	PCT-US94-12591-27	Sequence 27, Appl
413	56	60.9	32	1	US-08-470-846A-15	Sequence 15, Appl	486	47	51.1	29	4	PCT-US94-12591-28	Sequence 28, Appl
414	56	60.9	32	4	US-09-154-390-15	Sequence 15, Appl	487	46	50.0	23	1	US-07-781-590A-2	Sequence 2, Appli
415	56	60.9	32	4	PCT-US94-12591-15	Sequence 15, Appl	488	46	50.0	23	1	US-07-781-590A-6	Sequence 6, Appli
416	55.5	60.3	27	6	5204327-2	Patent No. 5204327	489	46	50.0	23	1	US-07-781-590A-10	Sequence 10, Appl
417	55	59.8	22	1	US-07-828-450-21	Sequence 21, Appl	490	46	50.0	23	1	US-07-781-590A-11	Sequence 11, Appl
418	55	59.8	27	1	US-07-828-450-30	Sequence 30, Appl	491	45	48.9	27	1	US-08-451-240-19	Sequence 19, Appl
419	55	59.8	28	1	US-08-451-240-12	Sequence 12, Appl	492	45	48.9	27	1	US-08-451-240-33	Sequence 33, Appl
420	55	59.8	28	1	US-08-451-240-13	Sequence 13, Appl	493	45	48.9	27	2	US-09-154-390-35	Sequence 35, Appl
421	55	59.8	28	1	US-08-470-846A-12	Sequence 12, Appl	494	45	48.9	27	2	US-09-154-390-36	Sequence 36, Appl
422	55	59.8	28	1	US-08-470-846A-13	Sequence 13, Appl	495	45	48.9	27	2	US-09-154-390-37	Sequence 37, Appl
423	55	59.8	28	2	US-09-154-390-12	Sequence 12, Appl	496	45	48.9	27	4	PCT-US94-12591-19	Sequence 19, Appl
424	55	59.8	28	2	PCT-US94-12591-13	Sequence 13, Appl	497	45	48.9	27	4	PCT-US94-12591-33	Sequence 33, Appl
425	55	59.8	28	4	PCT-US94-12591-12	Sequence 12, Appl	498	45	48.9	29	1	US-08-451-240-18	Sequence 18, Appl
426	55	59.8	28	4	PCT-US94-12591-13	Sequence 13, Appl	499	45	48.9	29	2	US-09-154-390-18	Sequence 18, Appl
427	55	59.8	32	4	US-08-954-915A-9	Sequence 9, Appli	500	45	48.9	29	2	PCT-US94-12591-18	Sequence 18, Appl
428	54	58.7	22	2	US-09-466-268B-11	Sequence 11, Appl	501	44	47.8	28	2	US-08-954-915A-50	Sequence 50, Appl
429	53	57.6	15	6	5212286-24	Sequence 24, Appl	502	43	46.7	21	2	US-08-522-269B-5	Sequence 5, Appli
430	52.5	57.1	22	6	5212286-57	Patent No. 5212286	503	43	46.7	21	2	US-09-294-923-5	Sequence 5, Appli
431	52	56.5	13	2	US-08-942-456-4	Sequence 4, Appli	504	43	46.7	23	1	US-08-522-269B-11	Sequence 11, Appl
432	52	56.5	13	2	US-09-510-721-4	Sequence 4, Appli	505	43	46.7	23	1	US-09-294-923-11	Sequence 3, Appli
433	52	56.5	21	2	US-08-942-332B-4	Sequence 4, Appli	506	43	46.7	677	1	US-08-522-269B-3	Sequence 3, Appli
434	52	56.5	21	2	US-09-623-548A-496	Sequence 496, App	507	43	46.7	677	1	US-09-294-923-3	Sequence 9, Appli
435	52	56.5	21	2	US-09-657-276-496	Sequence 496, App	508	41	44.6	45	1	US-07-728-221B-9	Sequence 9, Appli
436	52	56.5	22	1	US-07-781-590A-17	Sequence 17, Appl	509	41	44.6	51	2	US-09-270-767-40233	Sequence 40233, A
437	52	56.5	25	6	5212286-49	Patent No. 5212286	510	41	44.6	51	2	US-09-270-767-55449	Sequence 55449, A
438	51	55.4	28	1	US-08-451-240-26	Sequence 26, Appl	511	41	44.6	192	2	US-09-252-991A-20144	Sequence 20144, A
439	51	55.4	28	1	US-08-451-240-37	Sequence 37, Appl	512	41	44.6	307	2	US-09-854-133-397	Sequence 397, App
440	51	55.4	28	1	US-08-470-846A-28	Sequence 28, Appl	513	41	44.6	389	2	US-09-673-395A-487	Sequence 487, App
441	51	55.4	28	1	US-08-470-846A-33	Sequence 33, Appl	514	41	44.6	389	2	US-09-673-395A-621	Sequence 621, App
442	51	55.4	28	2	US-09-154-390-28	Sequence 28, Appl	515	41	44.6	399	2	US-09-673-395A-471	Sequence 471, App
443	51	55.4	28	4	PCT-US94-12591-26	Sequence 26, Appl	516	41	44.6	821	2	US-09-252-991A-21013	Sequence 21013, A
444	51	55.4	28	4	PCT-US94-12591-36	Sequence 36, Appl	517	40	43.5	79	2	US-09-902-540-11361	Sequence 11361, A
445	51	55.4	28	4	PCT-US94-12591-37	Sequence 37, Appl	518	40	43.5	328	2	US-09-270-767-42877	Sequence 42877, A
446	51	55.4	28	4	PCT-US94-12591-37	Sequence 37, Appl	519	40	43.5	593	2	US-09-302-626B-64	Sequence 64, Appl
447	50	54.3	28	1	US-08-451-240-36	Sequence 36, Appl	520	40	43.5	733	2	US-09-902-540-16379	Sequence 16379, A
448	50	54.3	28	2	US-09-154-390-40	Sequence 40, Appl	521	40	43.5	4866	2	US-09-424-783-2	Sequence 2, Appli
449	49	53.3	21	2	US-09-623-548A-494	Sequence 494, App	522	40	43.5	4872	2	US-09-424-783-3	Sequence 3, Appli
450	49	53.3	21	2	US-09-657-276-494	Sequence 494, App	523	39.5	42.9	1589	2	US-09-543-681A-4998	Sequence 4998, App
451	49	53.3	28	1	US-08-451-240-16	Sequence 16, Appl	524	39	42.4	28	1	US-08-470-846A-43	Sequence 47, Appl
452	49	53.3	28	1	US-08-451-240-32	Sequence 32, Appl	525	39	42.4	30	1	US-08-451-240-47	Sequence 47, Appl
453	49	53.3	28	1	US-08-451-240-35	Sequence 35, Appl	526	39	42.4	30	1	PCT-US94-12591-47	Sequence 47, Appl
454	49	53.3	28	1	US-08-470-846A-16	Sequence 16, Appl	527	39	42.4	162	2	US-09-270-767-45268	Sequence 45268, A
455	49	53.3	28	2	US-09-154-390-16	Sequence 16, Appl	528	39	42.4	261	2	US-09-252-991A-23172	Sequence 23172, A
456	49	53.3	28	2	US-09-154-390-34	Sequence 34, Appl	529	39	42.4	274	2	US-09-489-039A-10854	Sequence 10854, A
457	49	53.3	28	2	US-09-154-390-39	Sequence 39, Appl	530	39	42.4	363	2	US-09-949-016-10535	Sequence 10535, A
458	49	53.3	28	4	PCT-US94-12591-16	Sequence 16, Appl	531	39	42.4	1437	2	US-09-824-574-2	Sequence 2, Appli
459	49	53.3	28	4	PCT-US94-12591-32	Sequence 32, Appl	532	39	42.4	1466	2	US-08-286-819A-27	Sequence 27, Appl
460	49	53.3	28	4	PCT-US94-12591-35	Sequence 35, Appl	533	38.5	41.8	2296	1	US-08-980-357-27	Sequence 27, Appl
461	49	53.3	32	2	US-08-954-915A-10	Sequence 10, Appl	534	38.5	41.8	2296	2	US-09-357-375-27	Sequence 27, Appl
462	48	52.2	22	1	US-08-451-240-29	Sequence 29, Appl	535	38.5	41.8	2296	2	US-09-357-375-27	Sequence 27, Appl
463	48	52.2	22	1	US-08-451-240-30	Sequence 30, Appl	536	38	41.3	13	6	5212286-46	Patent No. 5212286
464	48	52.2	22	1	US-08-470-846A-21	Sequence 21, Appl	537	38	41.3	15	2	US-09-623-548A-493	Sequence 493, App
465	48	52.2	22	2	US-09-154-390-31	Sequence 31, Appl	538	38	41.3	15	2	US-09-657-276-493	Sequence 493, App

539	38	41.3	1	US-07-828-450-32	Sequence 32, Appl	612	36	39.1	41	1	US-07-924-753-1	Sequence 1, Appl
540	38	41.3	2	US-09-270-767-4457	Sequence 44357, A	613	36	39.1	46	2	US-09-270-767-44293	Sequence 44293, A
541	38	41.3	57	US-09-270-767-59779	Sequence 59779, A	614	36	39.1	54	1	US-08-563-148E-1	Sequence 1, Appl
542	38	41.3	74	US-09-134-000C-4144	Sequence 4144, Ap	615	36	39.1	98	2	US-09-194-139-9	Sequence 9, Appl
543	38	41.3	110	US-09-270-767-59166	Sequence 59166, A	616	36	39.1	107	2	US-09-538-092-92	Sequence 92, Appl
544	38	41.3	144	US-09-439-313-480	Sequence 480, App	617	36	39.1	112	2	US-09-902-540-16502	Sequence 16502, A
545	38	41.3	144	US-09-636-215-480	Sequence 480, App	618	36	39.1	133	1	US-07-924-753-15	Sequence 15, Appl
546	38	41.3	144	US-09-685-166A-480	Sequence 480, App	619	36	39.1	178	2	US-09-252-991A-17000	Sequence 17000, A
547	38	41.3	144	US-09-679-426-480	Sequence 480, App	620	36	39.1	221	2	US-09-902-540-15515	Sequence 15515, A
548	38	41.3	144	US-09-759-143-480	Sequence 480, App	621	36	39.1	230	2	US-10-101-464A-707	Sequence 707, App
549	38	41.3	144	US-09-651-236-480	Sequence 480, App	622	36	39.1	294	2	US-09-252-991A-27242	Sequence 27242, A
550	38	41.3	144	US-09-657-279-480	Sequence 480, App	623	36	39.1	338	2	US-09-538-092-1281	Sequence 1281, Ap
551	38	41.3	144	US-10-012-896-480	Sequence 480, App	624	36	39.1	338	2	US-09-949-016-7300	Sequence 7300, Ap
552	38	41.3	155	US-09-252-991A-28474	Sequence 28474, A	625	36	39.1	394	2	US-09-048-473-2	Sequence 2, Appl
553	38	41.3	190	US-09-270-767-43767	Sequence 43767, A	626	36	39.1	468	2	US-09-199-637A-29	Sequence 29, Appl
554	38	41.3	2283	US-10-172-502-4	Sequence 4, Appl	627	36	39.1	495	2	US-09-252-991A-26109	Sequence 26109, A
555	37	40.2	10	5212286-7	Patent No. 5212286	628	36	39.1	605	2	US-08-753-007A-2	Sequence 2, Appl
556	37	40.2	30	US-09-623-548A-22	Sequence 22, Appl	629	36	39.1	605	2	US-09-398-496-2	Sequence 2, Appl
557	37	40.2	30	US-09-657-276-22	Sequence 22, Appl	630	36	39.1	706	2	US-09-252-991A-32448	Sequence 32448, A
558	37	40.2	86	US-09-270-767-60103	Sequence 60103, A	631	36	39.1	728	2	US-09-747-259-18	Sequence 18, Appl
559	37	40.2	103	US-09-134-000C-4249	Sequence 4249, Ap	632	36	39.1	728	2	US-09-816-744-18	Sequence 18, Appl
560	37	40.2	159	US-09-252-991A-21183	Sequence 21183, A	633	36	39.1	728	2	US-10-104-047-3399	Sequence 3399, Ap
561	37	40.2	164	US-09-621-976-480A	Sequence 480A, Ap	634	36	39.1	733	2	US-09-073-587-3	Sequence 3, Appl
562	37	40.2	168	US-09-521-991A-21681	Sequence 21681, A	635	36	39.1	754	1	US-08-525-864B-2	Sequence 2, Appl
563	37	40.2	186	US-09-252-991A-30658	Sequence 30658, A	636	36	39.1	871	2	US-09-245-041-19	Sequence 19, Appl
564	37	40.2	188	US-09-489-039A-13345	Sequence 13345, A	637	36	39.1	871	2	US-09-358-055B-19	Sequence 19, Appl
565	37	40.2	241	US-10-360-101-223	Sequence 223, App	638	36	39.1	871	2	US-09-893-238-19	Sequence 19, Appl
566	37	40.2	246	US-10-104-047-2195	Sequence 2195, Ap	639	36	39.1	1045	2	US-09-252-991A-17661	Sequence 17661, A
567	37	40.2	267	US-09-949-016-6007	Sequence 6007, Ap	640	36	39.1	1350	2	US-09-245-041-17	Sequence 17, Appl
568	37	40.2	291	US-09-949-016-9125	Sequence 9125, Ap	641	36	39.1	1350	2	US-09-358-055B-17	Sequence 17, Appl
569	37	40.2	295	US-09-949-016-7683	Sequence 7683, Ap	642	36	39.1	1350	2	US-09-893-238-17	Sequence 17, Appl
570	37	40.2	327	US-08-679-493A-71	Sequence 71, Appl	643	35.5	38.6	146	2	US-09-732-210-1431	Sequence 1431, Ap
571	37	40.2	349	US-09-328-352-7078	Sequence 7078, Ap	644	35.5	38.6	154	2	US-09-489-039A-13897	Sequence 13897, A
572	37	40.2	361	US-09-810-836B-2	Sequence 2, Appl	645	35.5	38.6	485	1	US-08-453-956-15	Sequence 15, Appl
573	37	40.2	367	US-09-370-767-44650	Sequence 44650, A	646	35.5	38.6	485	1	US-08-086-631-15	Sequence 15, Appl
574	37	40.2	379	US-09-107-532A-3904	Sequence 3904, Ap	647	35.5	38.6	485	1	US-08-452-930-15	Sequence 15, Appl
575	37	40.2	513	US-10-012-231A-385	Sequence 385, App	648	35.5	38.6	485	2	US-10-010-065-2	Sequence 2, Appl
576	37	40.2	513	US-10-015-389A-385	Sequence 385, App	649	35.5	38.6	485	4	PCT-US93-08174-15	Sequence 15, Appl
577	37	40.2	513	US-10-006-768A-385	Sequence 385, App	650	35.5	38.6	801	2	US-09-270-767-44264	Sequence 44264, A
578	37	40.2	513	US-10-015-671A-385	Sequence 385, App	651	35	38.0	15	2	US-09-405-745-2	Sequence 2, Appl
579	37	40.2	513	US-10-015-393A-385	Sequence 385, App	652	35	38.0	28	1	US-08-202-525-1	Sequence 1, Appl
580	37	40.2	513	US-10-011-833A-385	Sequence 385, App	653	35	38.0	56	2	US-09-205-258-748	Sequence 748, App
581	37	40.2	513	US-10-006-041A-385	Sequence 385, App	654	35	38.0	56	2	US-10-004-860-748	Sequence 748, App
582	37	40.2	513	US-10-012-064A-385	Sequence 385, App	655	35	38.0	62	2	US-09-270-767-32593	Sequence 32593, A
583	37	40.2	536	US-09-902-540-10962	Sequence 10962, A	656	35	38.0	62	2	US-09-270-767-47810	Sequence 47810, A
584	37	40.2	557	US-09-489-039A-9672	Sequence 9672, Ap	657	35	38.0	99	2	US-09-950-933A-83	Sequence 83, Appl
585	37	40.2	561	US-09-949-016-8161	Sequence 8161, Ap	658	35	38.0	103	2	US-09-252-991A-16712	Sequence 16712, A
586	37	40.2	580	US-09-556-916-18	Sequence 18, Appl	659	35	38.0	111	2	US-08-899-330-5	Sequence 5, Appl
587	37	40.2	580	US-09-556-916-24	Sequence 24, Appl	660	35	38.0	111	2	US-08-756-541-5	Sequence 5, Appl
588	37	40.2	581	US-09-556-916-6	Sequence 6, Appl	661	35	38.0	151	2	US-09-732-210-1353	Sequence 1353, Ap
589	37	40.2	581	US-09-556-916-12	Sequence 12, Appl	662	35	38.0	155	2	US-09-543-681A-7630	Sequence 7630, Ap
590	37	40.2	626	US-09-556-916-14	Sequence 14, Appl	663	35	38.0	155	2	US-09-248-796A-25902	Sequence 25902, A
591	37	40.2	626	US-09-556-916-16	Sequence 16, Appl	664	35	38.0	156	2	US-09-270-767-34637	Sequence 34637, A
592	37	40.2	626	US-09-556-916-20	Sequence 20, Appl	665	35	38.0	156	2	US-09-270-767-49854	Sequence 49854, A
593	37	40.2	626	US-09-556-916-22	Sequence 22, Appl	666	35	38.0	159	2	US-09-270-767-41393	Sequence 41393, A
594	37	40.2	627	US-09-556-916-2	Sequence 2, Appl	667	35	38.0	159	2	US-09-270-767-56609	Sequence 56609, A
595	37	40.2	627	US-09-556-916-4	Sequence 4, Appl	668	35	38.0	172	2	US-09-252-991A-17189	Sequence 17189, A
596	37	40.2	627	US-09-556-916-8	Sequence 8, Appl	669	35	38.0	194	1	US-08-616-368A-11	Sequence 11, Appl
597	37	40.2	627	US-09-556-916-10	Sequence 10, Appl	670	35	38.0	194	2	US-09-054-298-11	Sequence 11, Appl
598	37	40.2	627	US-09-949-016-6840	Sequence 6840, Ap	671	35	38.0	194	2	US-08-818-655-11	Sequence 11, Appl
599	37	40.2	646	US-09-543-681A-6638	Sequence 6638, Ap	672	35	38.0	194	2	US-09-305-839-11	Sequence 11, Appl
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601	37	40.2	679	US-09-302-620B-84	Sequence 84, Appl	674	35	38.0	205	2	US-09-252-991A-25485	Sequence 25485, A
602	37	40.2	679	US-09-912-161-4	Sequence 4, Appl	675	35	38.0	216	2	US-09-252-991A-20124	Sequence 20124, A
603	37	40.2	679	US-09-912-161-6	Sequence 6, Appl	676	35	38.0	231	2	US-09-489-039A-14299	Sequence 14299, A
604	37	40.2	679	US-09-911-781-11	Sequence 11, Appl	677	35	38.0	234	2	US-09-252-991A-23005	Sequence 23005, A
605	37	40.2	679	US-10-400-902-11	Sequence 11, Appl	678	35	38.0	275	2	US-09-328-352-7552	Sequence 7552, Ap
606	37	40.2	819	US-09-651-656-15	Sequence 15, Appl	679	35	38.0	298	2	US-09-270-767-32340	Sequence 32340, A
607	37	40.2	819	US-09-650-855-15	Sequence 15, Appl	680	35	38.0	298	2	US-09-270-767-47557	Sequence 47557, A
608	37	40.2	945	US-09-248-796A-15743	Sequence 15743, A	681	35	38.0	315	2	US-09-270-767-43782	Sequence 43782, A
609	37	40.2	1075	PCT-US94-07297-41	Sequence 41, Appl	682	35	38.0	337	2	US-09-270-767-46773	Sequence 46773, A
610	37	40.2	5032	US-09-538-092-979	Sequence 979, App	683	35	38.0	365	2	US-09-949-016-7947	Sequence 7947, Ap
611	37	40.2	5037	US-09-424-783-4	Sequence 4, Appl	684	35	38.0	383	2	US-09-949-016-6053	Sequence 6053, Ap

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686	35	38.0	433	2	US-09-949-016-10233	Sequence 10233, A	759	34	37.0	367	2	US-09-778-427-2	Sequence 2, Appli
687	35	38.0	441	2	US-09-107-433-4780	Sequence 4780, A	760	34	37.0	368	2	US-09-198-452A-635	Sequence 635, App
688	35	38.0	448	2	US-09-134-000C-6746	Sequence 6746, Ap	761	34	37.0	368	2	US-09-438-185A-595	Sequence 595, App
689	35	38.0	479	2	US-09-252-991A-18876	Sequence 18876, A	762	34	37.0	371	2	US-09-501-115-14	Sequence 14, Appl
690	35	38.0	494	2	US-09-583-110-4005	Sequence 4005, Ap	763	34	37.0	371	2	US-10-357-886-14	Sequence 14, Appl
691	35	38.0	495	2	US-09-248-796A-14275	Sequence 14275, A	764	34	37.0	378	2	US-09-967-552A-38	Sequence 38, Appl
692	35	38.0	615	2	US-09-252-991A-27273	Sequence 27273, A	765	34	37.0	404	2	US-09-248-796A-16463	Sequence 16463, A
693	35	38.0	782	2	US-09-949-016-6943	Sequence 6943, Ap	766	34	37.0	406	2	US-09-252-991A-20630	Sequence 20630, A
694	35	38.0	793	2	US-09-949-016-6943	Sequence 6943, Ap	767	34	37.0	419	2	US-08-115-753-2	Sequence 33, Appl
695	35	38.0	869	2	US-09-489-039A-7727	Sequence 7727, Ap	768	34	37.0	419	2	US-08-115-753-33	Sequence 33, Appl
696	35	38.0	1016	2	US-09-949-016-11018	Sequence 11018, A	769	34	37.0	437	2	US-09-949-016-6542	Sequence 6542, Ap
697	35	38.0	1059	2	US-09-394-272-5	Sequence 5, Appli	770	34	37.0	439	2	US-08-952-457-2	Sequence 3, Appli
698	35	38.0	1140	1	US-08-657-641-7	Sequence 7, Appli	771	34	37.0	439	2	US-08-952-457-3	Sequence 3, Appli
699	35	38.0	1140	4	PCT-US94-07233-7	Sequence 7, Appli	772	34	37.0	443	2	US-09-949-016-11402	Sequence 11402, A
700	35	38.0	1166	2	US-10-104-047-2949	Sequence 2949, Ap	773	34	37.0	445	2	US-09-489-039A-13869	Sequence 13869, A
701	35	38.0	1495	2	US-09-543-681A-5986	Sequence 5986, Ap	774	34	37.0	460	2	US-09-198-452A-7	Sequence 7, Appli
702	35	38.0	1522	2	US-10-144-198-31	Sequence 31, Appl	775	34	37.0	460	2	US-09-438-185A-1071	Sequence 1071, Ap
703	35	38.0	4528	2	US-09-036-987A-5	Sequence 5, Appli	776	34	37.0	483	1	US-08-194-338-7	Sequence 7, Appli
704	35	38.0	4928	2	US-09-370-700-5	Sequence 5, Appli	777	34	37.0	543	2	US-09-252-991A-29830	Sequence 29830, A
705	35	38.0	4928	2	US-09-603-207-5	Sequence 5, Appli	778	34	37.0	546	1	US-08-942-423-4	Sequence 4, Appli
706	34.5	37.5	84	2	US-08-905-223-432	Sequence 432, App	779	34	37.0	546	2	US-08-630-915A-14	Sequence 14, Appl
707	34.5	37.5	134	2	US-09-640-211A-597	Sequence 597, App	780	34	37.0	546	2	US-09-879-957-14	Sequence 14, Appl
708	34.5	37.5	165	2	US-09-252-991A-31106	Sequence 31106, A	781	34	37.0	550	2	US-09-538-092-1324	Sequence 1324, Ap
709	34.5	37.5	311	1	US-08-794-216-1	Sequence 1, Appli	782	34	37.0	553	2	US-09-514-245-4	Sequence 4, Appli
710	34.5	37.5	311	2	US-09-520-781-18	Sequence 18, Appl	783	34	37.0	556	2	US-09-270-767-41922	Sequence 41922, A
711	34.5	37.5	311	2	US-09-957-187-18	Sequence 18, Appl	784	34	37.0	559	1	US-09-052-339-1	Sequence 1, Appli
712	34.5	37.5	311	2	US-09-991-053-18	Sequence 18, Appl	785	34	37.0	559	2	US-09-385-742B-1	Sequence 1, Appli
713	34.5	37.5	311	2	US-09-991-053-18	Sequence 18, Appl	786	34	37.0	559	2	US-09-989-786-1	Sequence 1, Appli
714	34.5	37.5	570	2	US-09-902-540-16111	Sequence 16111, A	787	34	37.0	559	2	US-09-807-123-2	Sequence 2, Appli
715	34.5	37.5	1245	2	US-09-252-991A-30935	Sequence 30935, A	788	34	37.0	622	2	US-09-252-991A-27587	Sequence 27587, A
716	34	37.0	27	2	US-09-364-956-43	Sequence 43, Appl	789	34	37.0	643	2	US-09-232-191-33	Sequence 33, Appl
717	34	37.0	43	2	US-09-027-108C-6	Sequence 6, Appli	790	34	37.0	643	2	US-09-232-191-33	Sequence 33, Appl
718	34	37.0	43	2	US-10-318-675-74	Sequence 74, Appl	791	34	37.0	643	2	US-09-232-197-83	Sequence 83, Appl
719	34	37.0	76	2	US-09-270-767-34207	Sequence 34207, A	792	34	37.0	643	2	US-09-232-201-83	Sequence 83, Appl
720	34	37.0	111	2	US-08-899-330-6	Sequence 6, Appli	793	34	37.0	643	2	US-09-232-195-83	Sequence 83, Appl
721	34	37.0	111	2	US-09-756-541-6	Sequence 6, Appli	794	34	37.0	659	2	US-09-626-589-2	Sequence 2, Appli
722	34	37.0	116	2	US-09-482-273-115	Sequence 115, App	795	34	37.0	676	2	US-09-003-574-34	Sequence 34, Appl
723	34	37.0	123	2	US-09-489-039A-7992	Sequence 7992, Ap	796	34	37.0	676	2	US-09-003-570-34	Sequence 34, Appl
724	34	37.0	127	2	US-09-489-039A-8856	Sequence 8856, Ap	797	34	37.0	676	2	US-09-864-541A-34	Sequence 34, Appl
725	34	37.0	127	2	US-09-270-767-5914	Sequence 5914, A	798	34	37.0	678	2	US-09-270-767-42257	Sequence 42257, A
726	34	37.0	132	2	US-09-589-892B-13	Sequence 13, Appl	799	34	37.0	708	2	US-09-857-556A-12	Sequence 12, Appl
727	34	37.0	133	2	US-09-270-767-39478	Sequence 39478, A	800	34	37.0	717	2	US-09-626-589-1	Sequence 1, Appli
728	34	37.0	133	2	US-09-270-767-54695	Sequence 54695, A	801	34	37.0	719	2	US-09-857-556A-33	Sequence 33, Appl
729	34	37.0	135	2	US-09-252-991A-28251	Sequence 28251, A	802	34	37.0	721	2	US-09-857-556A-10	Sequence 10, Appl
730	34	37.0	147	2	US-09-482-273-209	Sequence 209, App	803	34	37.0	824	2	US-09-626-589-3	Sequence 3, Appli
731	34	37.0	155	2	US-09-640-211A-2128	Sequence 2128, Ap	804	34	37.0	925	2	US-09-949-016-6086	Sequence 6086, Ap
732	34	37.0	188	2	US-09-270-767-40814	Sequence 40814, A	805	34	37.0	1013	2	US-09-062-126-3	Sequence 3, Appli
733	34	37.0	188	2	US-09-270-767-56030	Sequence 56030, A	806	34	37.0	1022	2	US-08-772-270A-2	Sequence 2, Appli
734	34	37.0	202	2	US-09-270-767-31876	Sequence 31876, A	807	34	37.0	1087	2	US-09-918-909A-24	Sequence 24, Appl
735	34	37.0	202	2	US-09-270-767-47093	Sequence 47093, A	808	34	37.0	1087	2	US-09-538-092-1033	Sequence 1033, Ap
736	34	37.0	202	2	US-09-248-796A-15465	Sequence 15465, A	809	34	37.0	1722	2	US-09-538-092-1033	Sequence 1033, Ap
737	34	37.0	204	2	US-09-489-039A-7643	Sequence 7643, Ap	810	34	37.0	2375	2	US-09-538-092-1131	Sequence 1131, Ap
738	34	37.0	210	1	US-08-320-559-4	Sequence 4, Appli	811	34	37.0	2476	2	US-09-824-574-7	Sequence 7, Appli
739	34	37.0	210	1	US-08-327-392-4	Sequence 4, Appli	812	33.5	36.4	135	1	US-08-687-916-20	Sequence 20, Appl
740	34	37.0	210	2	US-08-545-860D-4	Sequence 4, Appli	813	33.5	36.4	135	2	US-09-138-614-20	Sequence 20, Appl
741	34	37.0	210	4	PCT-US94-04496-4	Sequence 4, Appli	814	33.5	36.4	272	2	US-09-270-767-46084	Sequence 46084, A
742	34	37.0	268	2	US-09-270-767-32030	Sequence 32030, A	815	33.5	36.4	294	1	US-09-258-371-10	Sequence 10, Appl
743	34	37.0	269	2	US-09-270-767-46698	Sequence 46698, A	816	33.5	36.4	294	2	US-08-751-230-10	Sequence 10, Appl
744	34	37.0	271	2	US-09-270-767-44475	Sequence 44475, A	817	33.5	36.4	294	2	US-09-499-082-10	Sequence 10, Appl
745	34	37.0	272	2	US-09-199-637A-285	Sequence 285, App	818	33.5	36.4	294	2	US-09-258-372-10	Sequence 10, Appl
746	34	37.0	272	2	US-09-252-991A-21429	Sequence 21429, A	819	33.5	36.4	294	2	US-09-006-783A-3	Sequence 3, Appli
747	34	37.0	272	2	US-09-270-767-43982	Sequence 43982, A	820	33.5	36.4	294	2	US-09-159-871-2	Sequence 2, Appli
748	34	37.0	313	2	US-09-800-729-196	Sequence 196, App	821	33.5	36.4	294	2	US-09-442-013-12	Sequence 12, Appl
749	34	37.0	322	2	US-09-134-001C-5120	Sequence 5120, Ap	822	33.5	36.4	294	2	US-09-532-868-10	Sequence 10, Appl
750	34	37.0	327	1	US-08-907-674-3	Sequence 3, Appli	823	33.5	36.4	294	2	US-09-451-739H-19	Sequence 19, Appl
751	34	37.0	327	1	US-09-215-087-3	Sequence 3, Appli	824	33.5	36.4	294	2	US-09-602-362B-19	Sequence 19, Appl
752	34	37.0	327	2	US-09-391-959-3	Sequence 3, Appli	825	33.5	36.4	294	2	US-09-540-236-3296	Sequence 3296, Ap
753	34	37.0	327	2	US-09-252-991A-16998	Sequence 16998, A	826	33.5	36.4	342	2	US-09-940-016-7625	Sequence 7625, Ap
754	34	37.0	330	2	US-08-115-753-1	Sequence 1, Appli	827	33.5	36.4	342	2	US-09-949-016-9110	Sequence 9110, Ap
755	34	37.0	347	2	US-09-252-991A-19006	Sequence 19006, A	828	33.5	36.4	355	2	US-09-252-991A-23003	Sequence 23003, A
756	34	37.0	365	2	US-09-697-367-8	Sequence 8, Appli	829	33.5	36.4	491	1	US-08-687-916-23	Sequence 23, Appl
757	34	37.0	365	2	US-09-918-909A-8	Sequence 8, Appli	830	33.5	36.4	491	2	US-09-138-614-23	Sequence 23, Appl

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832	33.5	36.4	495	2	US-09-138-614-22	Sequence 22594, Appl	905	33	35.9	208	2	US-09-252-991A-31167	Sequence 31167, A
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834	33.5	36.4	1150	2	US-09-902-540-13969	Sequence 13969, A	907	33	35.9	210	2	US-09-181-183-8	Sequence 8, Appli
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839	33.5	36.4	1597	2	US-09-423-890-13	Sequence 13, Appl	912	33	35.9	228	2	US-08-896-933-25	Sequence 25, Appl
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842	33	35.9	19	2	US-09-294-923-10	Sequence 10, Appl	915	33	35.9	230	2	US-09-248-796A-27048	Sequence 27048, A
843	33	35.9	22	1	US-08-741-678-8	Sequence 8, Appli	916	33	35.9	231	2	US-09-248-796A-27586	Sequence 27586, A
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857	33	35.9	110	1	US-08-292-968-24	Sequence 24, Appl	930	33	35.9	279	2	US-09-277-700-34	Sequence 34, Appl
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879	33	35.9	153	2	US-08-974-549A-286	Sequence 286, App	952	33	35.9	414	2	US-09-315-355A-26	Sequence 26, Appl
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881	33	35.9	153	2	US-09-430-323-177	Sequence 177, App	954	33	35.9	418	2	US-09-826-509-535	Sequence 535, App
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979 33 35.9 555 1 US-08-588-258B-24 Sequence 24, Appl
980 33 35.9 555 2 US-08-460-505-24 Sequence 24, Appl
981 33 35.9 555 4 PCT-US96-08295-24 Sequence 24, Appl
982 33 35.9 558 2 US-09-949-016-7736 Sequence 7736, Ap
983 33 35.9 569 2 US-09-514-245-22 Sequence 22, Appl
984 33 35.9 629 2 US-09-489-039A-9904 Sequence 9904, Ap
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986 33 35.9 637 2 US-09-469-211A-4 Sequence 4, Appl
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992 33 35.9 642 2 US-09-328-352-5199 Sequence 5199, Ap
993 33 35.9 656 2 US-09-248-796A-27355 Sequence 27355, A
994 33 35.9 684 2 US-09-489-039A-13496 Sequence 13496, A
995 33 35.9 689 2 US-10-439-479-25 Sequence 25, Appl
996 33 35.9 692 2 US-09-003-574-31 Sequence 31, Appl
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999 33 35.9 705 2 US-09-538-092-626 Sequence 626, Ap
1000 33 35.9 720 2 US-08-899-437-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-850-910A-1
; Sequence 1, Application US/08850910A
; Patent No. 5948761
; GENERAL INFORMATION:
; APPLICANT: SEILHAMER, J. J.
; APPLICANT: LEWICKI, J.
; APPLICANT: SCARBOROUGH, R. M.
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
; PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER, LLP
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,910A
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/477,226
; FILING DATE: 08-FEB-1990
; APPLICATION NUMBER: 07/299,880
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 07/206,470
; FILING DATE: 14-JUN-1988
; APPLICATION NUMBER: 07/200,383
; FILING DATE: 31-MAY-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 219002025212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-850-910A-1

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Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
DB 4 CFGRKMDRISSSSGLGC 20

RESULT 2

US-10-106-806-7
; Sequence 7, Application US/10106806
; Patent No. 6818619
; GENERAL INFORMATION:
; APPLICANT: Burnett, Jr., John C.
; APPLICANT: Lisv, Ondrej
; TITLE OF INVENTION: Chimeric natriuretic peptides
; FILE REFERENCE: 150.1990S2
; CURRENT APPLICATION NUMBER: US/10/106,806
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 09/466,268
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-806-7

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Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
DB 10 CFGRKMDRISSSSGLGC 26

RESULT 3

US-09-902-517-1
; Sequence 1, Application US/09902517
; Patent No. 6897030
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
; NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383

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; PRIOR FILING DATE: 1988-05-31
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; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A portion of human ANP and pBNP.
US-09-902-517-1
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Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 CFGRKMDRISSSSGLGC 20

RESULT 4
US-07-828-450-41
; Sequence 41, Application US/07828450
; Patent No. 5434133
; GENERAL INFORMATION:
; APPLICANT: TANAKA, SHOJI
; APPLICANT: MINAMITAKE, YOSHIHARU
; APPLICANT: KITAJIMA, YASUO
; APPLICANT: FURUYA, MAYUMI
; APPLICANT: MATSUO, HISAYUKI
; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,450
; FILING DATE: 19920131
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 9437/94133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-828-450-41
Query Match 100.0%; Score 92; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26
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RESULT 5
US-08-297-330-2
; Sequence 2, Application US/08297330
; Patent No. 5583108
; GENERAL INFORMATION:
; APPLICANT: Wei, Chi-Ming
; APPLICANT: Burnett, John C.
; TITLE OF INVENTION: Vasonatin Peptide and Analogs
; TITLE OF INVENTION: Vasonatin Peptide and Analogs
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5583108west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-4131
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,330
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/025,935
; FILING DATE: 03-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 1016.99-US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mature human brain natriuretic peptide
; ORGANISM:
US-08-297-330-2
Query Match 100.0%; Score 92; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 6
US-08-451-240-3
; Sequence 3, Application US/08451240
; Patent No. 5665704
; GENERAL INFORMATION:
; APPLICANT: Lowe, David
; APPLICANT: Cunningham, Brian
; APPLICANT: Oare, David
; APPLICANT: McDowell, Robert S.
; APPLICANT: Burnier, John
; TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
; TITLE OF INVENTION: PEPTIDES
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,240
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362552
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0844P1C1
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-451-240-3
Query Match 100.0%; Score 92; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-08-451-240-3

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 7
US-08-451-240-22
Sequence 22, Application US/08451240
Patent No. 5665704
GENERAL INFORMATION:
APPLICANT: Lowe, David
APPLICANT: Cunningham, Brian
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,240
FILING DATE:
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362552
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0844P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-451-240-22
Query Match 100.0%; Score 92; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-08-451-240-22

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 8
US-08-470-846A-3
Sequence 3, Application US/08470846A
Patent No. 5846932
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Lowe, David G.
APPLICANT: Cunningham, Brian C.
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,846A
FILING DATE: 06-Jun-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419877
FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362552
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0844P2C1
TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-470-846A-3

Query Match          100.0%; Score 92; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 9
US-08-942-332B-1
; Sequence 1, Application US/08942332B
; Patent No. 6124430
; GENERAL INFORMATION:
; APPLICANT: MISCHAK, RONALD P.
; APPLICANT: LIM, GARRETT A.
; APPLICANT: SCARDINA, JAN M.
; TITLE OF INVENTION: ASSAY AND REAGENTS FOR QUANTIFYING HBNP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/942,332B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/610,172
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 21900-20280.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-942-456-1

Query Match          100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 11
US-09-510-721-1
; Sequence 1, Application US/09510721
; Patent No. 6376207
; GENERAL INFORMATION:
; APPLICANT: MISCHAK, RONALD P.
; APPLICANT: LIM, GARRETT A.
; APPLICANT: SCARDINA, JAN M.
; TITLE OF INVENTION: ASSAY AND REAGENTS FOR QUANTIFYING HBNP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/510,721
FILING DATE: 23-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/610,172
FILING DATE: 04-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 21900-20280.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-510-721-1
Query Match 100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 10 CFGRKMDRISSSSGLGC 26
RESULT 12
US-09-466-268B-6
Sequence 6, Application US/09466268B
Patent No. 6407211
GENERAL INFORMATION:
APPLICANT: Burnett, Jr., John C.
APPLICANT: Lisy, Ondrej
TITLE OF INVENTION: Chimeric natriuretic peptides
FILE REFERENCE: 150.199US1
CURRENT APPLICATION NUMBER: US/09/466,268B
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 32
TYPE: PRT
ORGANISM: Homo sapiens
US-09-466-268B-6
Query Match 100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 10 CFGRKMDRISSSSGLGC 26
RESULT 13
US-09-154-390-3
Sequence 3, Application US/09154390
Patent No. 6525022
GENERAL INFORMATION:
APPLICANT: Lowe, David G.
APPLICANT: Cunningham, Brian C.
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.

APPLICANT: Burnier, John P.
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
FILE REFERENCE: 13734.1USWS
CURRENT APPLICATION NUMBER: US/09/154,390
CURRENT FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: US 08/470,846
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/419,877
PRIOR FILING DATE: 1995-04-11
PRIOR APPLICATION NUMBER: US 08/362,552
PRIOR FILING DATE: 1995-01-06
PRIOR APPLICATION NUMBER: PCT/US94/12591
PRIOR FILING DATE: 1994-11-04
PRIOR APPLICATION NUMBER: US 08/152,994
PRIOR FILING DATE: 1993-11-12
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-154-390-3
Query Match 100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 10 CFGRKMDRISSSSGLGC 26
RESULT 14
US-09-154-390-22
Sequence 22, Application US/09154390
Patent No. 6525022
GENERAL INFORMATION:
APPLICANT: Lowe, David G.
APPLICANT: Cunningham, Brian C.
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John P.
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
FILE REFERENCE: 13734.1USWS
CURRENT APPLICATION NUMBER: US/09/154,390
CURRENT FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: US 08/470,846
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/419,877
PRIOR FILING DATE: 1995-04-11
PRIOR APPLICATION NUMBER: US 08/362,552
PRIOR FILING DATE: 1995-01-06
PRIOR APPLICATION NUMBER: PCT/US94/12591
PRIOR FILING DATE: 1994-11-04
PRIOR APPLICATION NUMBER: US 08/152,994
PRIOR FILING DATE: 1993-11-12
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-154-390-22
Query Match 100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17

Db 10 CFGRKMDRISSSSGLGC 26
|||||

RESULT 15
US-10-106-806-6
; Sequence 6, Application US/10106806
; Patent No. 6818619
; GENERAL INFORMATION:
; APPLICANT: Burnett, Jr., John C.
; APPLICANT: Lisy, Ondrej
; TITLE OF INVENTION: Chimeric natriuretic peptides
; FILE REFERENCE: 150.199US2
; CURRENT APPLICATION NUMBER: US/10/106,806
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 09/466,268
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-806-6

Query Match 100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
|||||

Db 10 CFGRKMDRISSSSGLGC 26
|||||

RESULT 16
US-09-623-548A-509
; Sequence 509, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thiбаudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 509
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-509

Query Match 100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17

Db 10 CFGRKMDRISSSSGLGC 26
|||||

RESULT 17
US-09-623-548A-516
; Sequence 516, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thiбаudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 516
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-516

Query Match 100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
|||||

Db 10 CFGRKMDRISSSSGLGC 26
|||||

RESULT 18
US-09-657-276-509
; Sequence 509, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thiбаudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 509

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; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-509

Query Match      100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CFGRKMDRISSSSGLGC 17
Db      10 CFGRKMDRISSSSGLGC 26

RESULT 19
US-09-657-276-516
; Sequence 516, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudreau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 516
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-516

Query Match      100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CFGRKMDRISSSSGLGC 17
Db      10 CFGRKMDRISSSSGLGC 26

RESULT 20
US-09-902-517-49
; Sequence 49, Application US/09902517
; Patent No. 6897030
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
; TITLE OF INVENTION: NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
```

```
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: R2
US-09-902-517-49

Query Match      100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CFGRKMDRISSSSGLGC 17
Db      10 CFGRKMDRISSSSGLGC 26

RESULT 21
PCT-US94-02391-2
; Sequence 2, Application PC/TUS9402391
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: 200 First Street S.W. 55905 USA
; APPLICANT: Rochester, Minnesota
; TITLE OF INVENTION: Vasonatin Peptide and Analogs Thereof
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02391
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/025,935
; FILING DATE: 03-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 150.99US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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MOLECULE TYPE: peptide
PCT-US94-02391-2

Query Match 100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSGLGC 17
Db 10 CFCGRKMDRISSSSGLGC 26

RESULT 22

PCT-US94-12591-3
Sequence 3, Application PC/TUS9412591

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Lowe, David
APPLICANT: Cunningham, Brian C.
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12591
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Daryl B.
REGISTRATION NUMBER: 32,637
REFERENCE/DOCKET NUMBER: 844P1
TELEPHONE: 415/225-1249
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-12591-3

Query Match 100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSGLGC 17
Db 10 CFCGRKMDRISSSSGLGC 26

RESULT 23

PCT-US94-12591-22
Sequence 22, Application PC/TUS9412591

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.

APPLICANT: Lowe, David
APPLICANT: Cunningham, Brian C.
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12591
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Daryl B.
REGISTRATION NUMBER: 32,637
REFERENCE/DOCKET NUMBER: 844P1
TELEPHONE: 415/225-1249
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-12591-22

Query Match 100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSGLGC 17
Db 10 CFCGRKMDRISSSSGLGC 26

RESULT 24

US-09-942-709-1
Sequence 1, Application US/09942709
Patent No. 6677124

GENERAL INFORMATION:
APPLICANT: TSUJI, Tetsuo
APPLICANT: INOUE, Ken
APPLICANT: YAMAUCHI, Akira
APPLICANT: KONO, Masao
APPLICANT: IGANO, Ken'ichi
TITLE OF INVENTION: Monoclonal Antibody Recognizing C-terminus of hBNP
FILE REFERENCE: 0039-0262P
CURRENT APPLICATION NUMBER: US/09/942,709
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: JP 3-326961
PRIOR FILING DATE: 1991-11-14
PRIOR APPLICATION NUMBER: US 07/976,457
PRIOR FILING DATE: 1992-11-13
PRIOR APPLICATION NUMBER: US 08/236,013
PRIOR FILING DATE: 1994-05-02
PRIOR APPLICATION NUMBER: US 08/749,031
PRIOR FILING DATE: 1996-11-14

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; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amino acid according to the usual solid phase method
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal BOC modified side chain Br-Z modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)..(2)
; OTHER INFORMATION: side chain Bzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(4)
; OTHER INFORMATION: side chain Cl-Z modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)..(9)
; OTHER INFORMATION: side chain Bzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)..(11)
; OTHER INFORMATION: side chain 4-CH3OBzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (14)..(14)
; OTHER INFORMATION: side chain TOS modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (15)..(15)
; OTHER INFORMATION: side chain Cl-Z modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (17)..(17)
; OTHER INFORMATION: side chain OCHex modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)..(20)
; OTHER INFORMATION: side chain Bzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (21)..(21)
; OTHER INFORMATION: side chain Bzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (22)..(22)
; OTHER INFORMATION: side chain Bzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (23)..(23)
; OTHER INFORMATION: side chain Bzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (27)..(27)
; OTHER INFORMATION: side chain 4-CH3OBzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (28)..(28)
; OTHER INFORMATION: side chain Cl-Z modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (31)..(31)
; OTHER INFORMATION: side chain TOS modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (32)..(32)
; OTHER INFORMATION: side chain TOS modified
; FEATURE:
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; NAME/KEY: SITE
; LOCATION: (33)..(33)
; OTHER INFORMATION: side chain Bom modified
US-09-942-709-1

Query Match      100.0%; Score 92; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 11 CFGRKMDRISSSSGLGC 27

RESULT 25
US-09-466-268B-1
; Sequence 1, Application US/09466268B
; Patent No. 6407211
; GENERAL INFORMATION:
; APPLICANT: Burnett, Jr., John C.
; APPLICANT: Lisy, Ondrej
; TITLE OF INVENTION: Chimeric natriuretic peptides
; FILE REFERENCE: 150.199US1
; CURRENT APPLICATION NUMBER: US/09/466,268B
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A chimeric peptide
US-09-466-268B-1

Query Match      100.0%; Score 92; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 26
US-10-106-806-1
; Sequence 1, Application US/10106806
; Patent No. 6818619
; GENERAL INFORMATION:
; APPLICANT: Burnett, Jr., John C.
; APPLICANT: Lisy, Ondrej
; TITLE OF INVENTION: Chimeric natriuretic peptides
; FILE REFERENCE: 150.199US2
; CURRENT APPLICATION NUMBER: US/10/106,806
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 09/466,268
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A chimeric peptide
US-10-106-806-1

Query Match      100.0%; Score 92; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 11 CFGRKMDRISSSSGLGC 27
```

Db 10 CFGRKMDRISSSSGLGC 26

RESULT 27

US-08-850-910A-45
; Sequence 45, Application US/08850910A
; Patent No. 5948761
; GENERAL INFORMATION:
; APPLICANT: SEILHAMER, J.J.
; APPLICANT: LEWICKI, J.
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER, LLP
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,910A
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/477,226
; FILING DATE: 08-FEB-1990
; APPLICATION NUMBER: 07/299,880
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 07/206,470
; FILING DATE: 14-JUN-1988
; APPLICATION NUMBER: 07/200,383
; FILING DATE: 31-MAY-1988
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 219002025212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-850-910A-45

Query Match 100.0%; Score 92; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17

Db 112 CFGRKMDRISSSSGLGC 128

RESULT 28

US-08-850-910A-48
; Sequence 48, Application US/08850910A
; Patent No. 5948761
; GENERAL INFORMATION:
; APPLICANT: SEILHAMER, J.J.
; APPLICANT: LEWICKI, J.

; APPLICANT: SCARBOROUGH, R.M.
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER, LLP
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,910A
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/477,226
; FILING DATE: 08-FEB-1990
; APPLICATION NUMBER: 07/299,880
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 07/206,470
; FILING DATE: 14-JUN-1988
; APPLICATION NUMBER: 07/200,383
; FILING DATE: 31-MAY-1988
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 219002025212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-850-910A-48

Query Match 100.0%; Score 92; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17

Db 112 CFGRKMDRISSSSGLGC 128

RESULT 29

US-09-508-435A-2
; Sequence 2, Application US/09508435A
; Patent No. 6828107
; GENERAL INFORMATION:
; APPLICANT: Shionogi & Co., Ltd.
; TITLE OF INVENTION: Immunoassay for BNP
; FILE REFERENCE: 2000-0259A/JJF/WMC/00177
; CURRENT APPLICATION NUMBER: US/09/508,435A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: JP 246684/1997
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: word (MS-DOS text)
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: human

```

US-09-508-435A-2
Query Match      100.0%; Score 92; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   |||||
Db 112 CFGRKMDRISSSSGLGC 128

RESULT 30
US-09-902-517-45
; Sequence 45, Application US/09902517
; Patent No. 6897030
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
; TITLE OF INVENTION: NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Deduced amino acid sequence of the human NRP
; OTHER INFORMATION: Comparison sequence of the prepro forms of the
US-09-902-517-48
Query Match      100.0%; Score 92; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   |||||
Db 112 CFGRKMDRISSSSGLGC 128

RESULT 32
US-09-623-548A-515
; Sequence 515, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 515
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-515
Query Match      97.8%; Score 90; DB 2; Length 33;
Best Local Similarity 94.1%; Pred. No. 1.1e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   |||||
Db 11 CFGRKMDRISSSSGLGC 27

RESULT 33
US-09-508-435A-2
Query Match      100.0%; Score 92; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   |||||
Db 112 CFGRKMDRISSSSGLGC 128

RESULT 31
US-09-902-517-48
; Sequence 48, Application US/09902517
; Patent No. 6897030
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
; TITLE OF INVENTION: NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910

```

US-09-657-276-515
; Sequence 515, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibault, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 515
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-515

Query Match 97.8%; Score 90; DB 2; Length 33;
Best Local Similarity 94.1%; Pred. No. 1.1e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 11 CFGRKMDRISSSSGLGC 27

RESULT 34
US-08-954-915A-1
; Sequence 1, Application US/08954915A
; Patent No. 6028055
; GENERAL INFORMATION:
; APPLICANT: Lowe, David
; APPLICANT: Schoenfeld, Jill
; TITLE OF INVENTION: Receptor Selective BNP
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,915A
; FILING DATE: 21-Oct-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/028854
; FILING DATE: 22-Oct-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575

REFERENCE/DOCKET NUMBER: P1017R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8228
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-954-915A-1

Query Match 95.7%; Score 88; DB 2; Length 32;
Best Local Similarity 94.1%; Pred. No. 2.3e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 35
US-09-466-268B-7
; Sequence 7, Application US/09466268B
; Patent No. 6407211
; GENERAL INFORMATION:
; APPLICANT: Burnett, Jr., John C.
; APPLICANT: Lisy, Ondrej
; TITLE OF INVENTION: Chimeric natriuretic peptides
; FILE REFERENCE: 150.199US1
; CURRENT APPLICATION NUMBER: US/09/466,268B
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-466-268B-7

Query Match 90.2%; Score 83; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLG 16
Db 10 CFGRKMDRISSSSGLG 25

RESULT 36
US-08-954-915A-4
; Sequence 4, Application US/08954915A
; Patent No. 6028055
; GENERAL INFORMATION:
; APPLICANT: Lowe, David
; APPLICANT: Schoenfeld, Jill
; TITLE OF INVENTION: Receptor Selective BNP
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,915A
; FILING DATE: 21-Oct-1997
; CLASSIFICATION: 514

1 CFGRKMDRISSSSGLGC 17
Ov

RESULT 39
US-08-954-915A-5
; Sequence 5, Application US/08954915A
; Patent No. 6028055
; GENERAL INFORMATION:
; APPLICANT: Lowe, David
; APPLICANT: Schoenfeld, Jill
; TITLE OF INVENTION: Receptor Selective BNP
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,915A
; FILING DATE: 21-Oct-1997
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/028854
; FILING DATE: 22-Oct-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P1017R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8228
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 32 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-954-915A-5

Query Match      84.8%; Score 78; DB 2; Length 32;
Best Local Similarity 82.4%; Pred. No. 1.2e-06;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFCGRKMDIRSSSSGLGC 17
Db 10 CFCGRKMDIRSSSSGLGC 26

RESULT 40
US-08-954-915A-24
; Sequence 24, Application US/08954915A
; Patent No. 6028055
; GENERAL INFORMATION:
; APPLICANT: Lowe, David
; APPLICANT: Schoenfeld, Jill
; TITLE OF INVENTION: Receptor Selective BNP
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,915A
; FILING DATE: 21-Oct-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/028854
; FILING DATE: 22-Oct-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P1017R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8228
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-954-915A-49

Query Match      83.7%; Score 77; DB 2; Length 32;
Best Local Similarity 82.4%; Pred. No. 1.9e-06;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFCGRKMDIRSSSSGLGC 17
Db 10 CFCGRKMDIRSSSSGLGC 26

RESULT 42
US-08-850-910A-15
; Sequence 15, Application US/08850910A
; Patent No. 5948761
; GENERAL INFORMATION:
; APPLICANT: SEILHAWER, J.J.
; APPLICANT: LEWICKI, J.
; APPLICANT: SCARBOROUGH, R.M.
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER, LLP
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,910A
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/477,226
; FILING DATE: 08-FEB-1990
```

APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-850-910A-15

Query Match 82.6%; Score 76; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.4e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 1 CFGRRLDRIGSLGSLGC 17

RESULT 43
US-09-902-517-15
Sequence 15, Application US/09902517
Patent No. 6897030
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Lewicki, John
APPLICANT: Scarborough, Robert M.
APPLICANT: Porter, Gordon J.
TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
NATRIURETIC PEPTIDE
FILE REFERENCE: 219002025213
CURRENT APPLICATION NUMBER: US/09/902,517
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 09/287,892
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: 08/850,910
PRIOR FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: 07/477,226
PRIOR FILING DATE: 1990-02-08
PRIOR APPLICATION NUMBER: 07/299,880
PRIOR FILING DATE: 1989-01-19
PRIOR APPLICATION NUMBER: 07/206,470
PRIOR FILING DATE: 1988-06-14
PRIOR APPLICATION NUMBER: 07/200,383
PRIOR FILING DATE: 1988-05-31
NUMBER OF SEQ IDS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 17
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Proviso formula (1)
US-09-902-517-15

Query Match 82.6%; Score 76; DB 2; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.4e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17

Db 1 CFGRRLDRIGSLGSLGC 17

RESULT 44
US-08-850-910A-34
Sequence 34, Application US/08850910A
Patent No. 5948761
GENERAL INFORMATION:
APPLICANT: SEILHAMER, J.J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-850-910A-34

Query Match 82.6%; Score 76; DB 1; Length 20;
Best Local Similarity 76.5%; Pred. No. 1.7e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 3 CFGRRLDRIGSLGSLGC 19

RESULT 45
US-09-902-517-34
Sequence 34, Application US/09902517
Patent No. 6897030
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Lewicki, John

APPLICANT: Scarborough, Robert M.
APPLICANT: Porter, Gordon J.
TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
TITLE OF INVENTION: NATRIURETIC PEPTIDE
FILE REFERENCE: 219002025213
CURRENT APPLICATION NUMBER: US/09/902,517
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 09/287,892
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: 08/850,910
PRIOR FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: 07/477,226
PRIOR FILING DATE: 1990-02-08
PRIOR APPLICATION NUMBER: 07/299,880
PRIOR FILING DATE: 1989-01-19
PRIOR APPLICATION NUMBER: 07/206,470
PRIOR FILING DATE: 1988-06-14
PRIOR APPLICATION NUMBER: 07/200,383
PRIOR FILING DATE: 1988-05-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Amino acids encoding pBNP
US-09-902-517-34

Query Match 82.6%; Score 76; DB 2; Length 20;
Best Local Similarity 76.5%; Pred. No. 1.7e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
||||:|||||
Db 3 CFGRRLDRIGLSGLGC 19

RESULT 46
US-07-828-450-10
Sequence 10, Application US/07828450
Patent No. 5434133
GENERAL INFORMATION:
APPLICANT: TANAKA, SHOJI
APPLICANT: MINAMITAKE, YOSHIHARU
APPLICANT: KITAJIMA, YASUO
APPLICANT: FURUYA, MAYUMI
APPLICANT: MATSUO, HISAYUKI
TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1625 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,450
FILING DATE: 19920131
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 9437/94133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944

TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-828-450-10

Query Match 82.6%; Score 76; DB 1; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
||||:|||||
Db 6 CFGLKMDRIGSMGLGC 22

RESULT 47
US-07-828-450-13
Sequence 13, Application US/07828450
Patent No. 5434133
GENERAL INFORMATION:
APPLICANT: TANAKA, SHOJI
APPLICANT: MINAMITAKE, YOSHIHARU
APPLICANT: KITAJIMA, YASUO
APPLICANT: FURUYA, MAYUMI
APPLICANT: MATSUO, HISAYUKI
TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1625 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,450
FILING DATE: 19920131
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 9437/94133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-828-450-13

Query Match 82.6%; Score 76; DB 1; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
||||:|||||
Db 6 CFGRKMDRIGSMGLGC 22

Query Match 82.6%; Score 76; DB 2; Length 26;
Best Local Similarity 76.5%; Pred. NO. 2.2e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFCRKWDRISSSSGLGC 17
Db 4 CFCRLDRIGSLGLGC 20

Search completed: January 25, 2006, 18:48:37
Job time : 27 secs

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OM protein - protein search, using sw model

Run on: January 25, 2006, 18:42:01 ; Search time 82 Seconds
(without alignments)
91.091 Million cell updates/sec

Title: US-10-737-290-172
Perfect score: 92
Sequence: 1 CPGKXMDRISSSGLGC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	17	ADL22372	Natriuret
2	92	100.0	17	ADL22373	Natriuret
3	92	100.0	17	AEb12959	Humaf bra
4	92	100.0	18	ADL22374	Natriuret
5	92	100.0	23	ADL22365	Natriuret
6	92	100.0	23	ADL22362	Natriuret
7	92	100.0	23	ADL22364	Natriuret
8	92	100.0	23	ADL22361	Natriuret
9	92	100.0	24	AAB46799	Humah bra
10	92	100.0	24	ADL22366	Natriuret
11	92	100.0	24	ADL22363	Natriuret
12	92	100.0	25	ADL22352	Natriuret
13	92	100.0	26	AAy67295	Humah bra
14	92	100.0	26	ABU63216	N-tefminu
15	92	100.0	26	ADL22354	Natriuret
16	92	100.0	26	ADP49303	Natriuret
17	92	100.0	26	ADP49273	Natriuret
18	92	100.0	26	ADW45317	Humah fus
19	92	100.0	26	ADY62994	Human bra
20	92	100.0	27	ADP49289	Natriuret
21	92	100.0	27	ADW45318	Human fus
22	92	100.0	27	ADW45367	Human BNP
23	92	100.0	28	ADW45365	Human BNP
24	92	100.0	28	ADW45319	Human fus

25	92	100.0	29	ADP49272	Natriuret
26	92	100.0	29	ADP49302	Natriuret
27	92	100.0	29	ADW45311	Human fus
28	92	100.0	29	ADW45310	Human fus
29	92	100.0	31	ADP49302	Mutated B
30	92	100.0	32	ADP49302	Mutated h
31	92	100.0	32	ADP49302	Mutated h
32	92	100.0	32	ADP49302	Mutated h
33	92	100.0	32	ADP49302	Mutated h
34	92	100.0	32	ADP49302	Mutated h
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66	92	100.0	32	ADP49302	Mutated h
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72	92	100.0	32	ADP49302	Mutated h
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93	92	100.0	32	ADP49302	Mutated h
94	92	100.0	32	ADP49302	Mutated h
95	92	100.0	32	ADP49302	Mutated h
96	92	100.0	32	ADP49302	Mutated h
97	92	100.0	32	ADP49302	Mutated h

98	92	100.0	118	6	ABR96183	Human NOV	171	82	89.1	32	2	AAW51305	Human B-t
99	92	100.0	121	8	ADM57400	Protein p	172	82	89.1	32	3	AAV80213	Human B-t
100	92	100.0	129	9	AEb63486	HUMNATPEP	173	81	88.0	17	8	ADP49292	Natriuret
101	92	100.0	134	2	AAR06603	Human Bra	174	81	88.0	32	8	ADL92006	Brain nat
102	92	100.0	134	2	AAR04087	Protein e	175	78	84.8	17	5	ABG98269	Human C-t
103	92	100.0	134	2	AAV05325	Human gam	176	78	84.8	32	2	AAW51262	Human B-t
104	92	100.0	134	4	AAE45735	Human BNP	177	78	84.8	32	2	AAW51281	Human B-t
105	92	100.0	134	7	ADG93293	Human pre	178	78	84.8	32	3	AAV80251	Human B-t
106	92	100.0	134	7	ADf16190	Human alb	179	78	84.8	32	3	AAV80234	Human B-t
107	92	100.0	134	8	ADM41413	Human bra	180	77	83.7	15	8	ADJ79684	Human Bra
108	92	100.0	134	8	ADQ30872	Human pre	181	77	83.7	21	2	AAW25774	Human Bra
109	92	100.0	134	8	ADR75283	Human bra	182	77	83.7	32	3	AAW51306	Human B-t
110	92	100.0	134	8	ADS54317	Human B-t	183	77	83.7	32	3	AAV80214	Human B-t
111	92	100.0	134	8	ADU05012	Amino aci	184	76	82.6	22	2	AAV29721	CNP analo
112	92	100.0	134	8	ADU04661	Human bra	185	76	82.6	22	2	AAV25955	CNP analo
113	92	100.0	134	8	ADY34278	Human bra	186	76	82.6	26	2	AAV04816	Peptide w
114	92	100.0	134	9	ADZ22718	Human pre	187	76	82.6	26	2	AAV04812	Peptide a
115	92	100.0	134	9	AEb63456	HUMNATPEP	188	76	82.6	26	4	AAV91335	Brain nat
116	92	100.0	143	9	ADW08049	Human bra	189	76	82.6	32	2	AAW70092	Brain nat
117	92	100.0	162	9	ADW08048	Human bra	190	76	82.6	32	2	AAW51301	Canine B-
118	92	100.0	162	9	AEb63457	HUMNATPEP	191	76	82.6	32	2	AAW51302	Porcine B
119	92	100.0	175	2	AAV72812	Gamma-IFN	192	76	82.6	32	3	AAV80221	Canine B-
120	92	100.0	197	8	ADM57398	Protein p	193	76	82.6	32	3	AAV80222	Porcine B
121	92	100.0	630	9	ADW45230	Human inv	194	76	82.6	32	4	AAV91331	Atrial-na
122	92	100.0	631	9	ADW45231	Human inv	195	76	82.6	32	4	AAV91336	Brain nat
123	92	100.0	632	9	ADW45232	Human inv	196	76	82.6	32	4	AAV45736	Canine BN
124	92	100.0	633	9	ADW45224	Human alb	197	76	82.6	32	4	AAE12436	Pig brain
125	92	100.0	641	7	ADf16537	Human alb	198	76	82.6	32	6	ADA09512	Human bra
126	92	100.0	641	9	ADW45226	Human ser	199	76	82.6	32	8	ADP49281	Natriuret
127	92	100.0	641	9	ADW45207	Human ser	200	76	82.6	32	8	ADP49301	Natriuret
128	92	100.0	661	9	ADW45277	Human ser	201	76	82.6	32	9	ADV86893	Beta BNP
129	92	100.0	663	9	ADW45280	Human ser	202	76	82.6	131	2	AAV07342	Porcine B
130	92	100.0	665	9	ADW45278	Human ser	203	76	82.6	131	2	AAV04084	Oligopept
131	92	100.0	667	9	ADW45223	Human ser	204	76	82.6	131	2	AAV04086	Protein e
132	92	100.0	670	9	ADW45229	Consensus	205	76	82.6	131	7	ADD93294	Pig prepr
133	92	100.0	673	9	ADW45197	Human ser	206	76	82.6	131	8	ADM41432	Pig brain
134	92	100.0	673	9	ADW45213	Human ser	207	76	82.6	140	6	ADA09507	Canine br
135	92	100.0	673	9	ADW45227	Human ser	208	76	82.6	140	8	ADM41417	Canine br
136	92	100.0	719	9	ADf16188	Human alb	209	76	82.6	169	9	ADM08082	Dog brain
137	90	97.8	33	4	AAV91339	Brain nat	210	75	81.5	17	5	ABG98211	Human C-t
138	89	96.7	19	8	ADP49298	Natriuret	211	75	81.5	28	6	ADA00827	Human hAN
139	89	96.7	24	8	ADP49306	Natriuret	212	74	80.4	17	5	ABG98241	Human C-t
140	89	96.7	32	8	ADL22378	Natriuret	213	74	80.4	17	5	ABG98268	Human C-t
141	89	96.7	32	8	ADL22379	Natriuret	214	74	80.4	17	5	ABG98270	Human C-t
142	89	96.7	33	8	ADL22380	Natriuret	215	74	80.4	22	2	AAV29914	CNP analo
143	88	95.7	17	8	ADL22369	Natriuret	216	74	80.4	22	2	AAV29720	CNP analo
144	88	95.7	17	8	ADL22370	Natriuret	217	74	80.4	25	2	AAV40711	[Lys134]h
145	88	95.7	18	8	ADL22371	Natriuret	218	74	80.4	25	2	AAV42952	Polypepti
146	88	95.7	23	8	ADL22358	Natriuret	219	74	80.4	28	6	ADA00822	Human hAN
147	88	95.7	23	8	ADL22359	Natriuret	220	74	80.4	32	3	AAV51273	Human B-t
148	88	95.7	24	8	ADL22360	Natriuret	221	74	80.4	32	3	AAV80243	Human B-t
149	88	95.7	25	8	ADL22356	Natriuret	222	74	80.4	37	2	AAW65450	Lebectin d
150	88	95.7	25	8	ADL22355	Natriuret	223	74	80.4	38	2	AAW65449	Lebectin d
151	88	95.7	26	8	ADL22357	Natriuret	224	74	80.4	46	2	AAW65444	Lebectin d
152	88	95.7	32	2	AAW51258	Human B-t	225	73	79.3	15	8	ADJ79683	Human Bra
153	88	95.7	32	3	AAV80212	Human B-t	226	73	79.3	17	5	AAV25952	CNP analo
154	88	95.7	32	8	ADL22376	Natriuret	227	73	79.3	17	5	ABG98203	Human C-t
155	88	95.7	32	8	ADL22387	Natriuret	228	73	79.3	17	6	ABG98267	Human C-t
156	88	95.7	32	8	ADL22375	Natriuret	229	73	79.3	17	5	ABG98203	Human C-t
157	88	95.7	33	8	ADL22377	Natriuret	230	73	79.3	22	2	AAV14792	C-type na
158	86	93.5	19	8	ADP49259	Natriuret	231	73	79.3	22	2	AAV29726	CNP analo
159	86	93.5	25	8	ADP49282	Natriuret	232	73	79.3	22	2	AAV29726	CNP analo
160	86	93.5	30	8	ADP49258	Natriuret	233	73	79.3	22	2	AAV29729	CNP analo
161	86	93.5	32	8	ADL22386	Natriuret	234	73	79.3	22	2	AAV29724	CNP analo
162	86	93.5	32	8	ADP49290	Natriuret	235	73	79.3	22	2	AAV25953	CNP analo
163	86	93.5	32	8	ADP49291	Natriuret	236	73	79.3	22	2	AAV32254	Human CNP
164	86	93.5	33	8	ADP49293	Natriuret	237	73	79.3	22	2	AAV21992	Porcine C
165	85	92.4	32	8	ADL22382	Natriuret	238	73	79.3	22	3	AAV24081	Human PRO
166	85	92.4	32	8	ADL22381	Natriuret	239	73	79.3	22	3	AAV10487	Human CNP
167	85	92.4	35	8	ADL22383	Natriuret	240	73	79.3	22	4	AAV82551	Human C-t
168	83	90.2	25	4	AAV82547	Human bra	241	73	79.3	22	4	AAV91341	C-type na
169	83	90.2	32	2	AAW51261	Type-B br	242	73	79.3	22	4	AAV91341	C-type na
170	83	90.2	32	3	AAV80208	Human B-t	243	73	79.3	22	4	AAV45741	Human C-t

244	73	79.3	22	4	AAB12439	C-type na	317	72	78.3	20	2	AAR40434	[D-Ala133
245	73	79.3	22	4	AAB70811	Human nat	318	72	78.3	21	2	AAR40623	[Arg129] [
246	73	79.3	22	5	ABG98202	Human C-t	319	72	78.3	21	2	AAR24330	Brain pep
247	73	79.3	22	6	ADA00766	Human nat	320	72	78.3	22	2	AAR29730	CNP analo
248	73	79.3	22	6	ABU63217	N-terminu	321	72	78.3	22	2	AAR29731	CNP analo
249	73	79.3	22	6	ADU63218	Human C-t	322	72	78.3	22	4	AAB91332	Brain nat
250	73	79.3	22	8	ADP49287	Natriuret	323	72	78.3	22	4	AAB91342	C-type na
251	73	79.3	22	9	ADW08064	Human bra	324	72	78.3	22	4	AAB91342	C-type na
252	73	79.3	22	9	ADY62996	Human C-t	325	72	78.3	22	4	AAB91342	C-type na
253	73	79.3	22	9	ADY62995	Human C-t	326	72	78.3	23	2	AAR40432	[Arg129] [
254	73	79.3	23	4	AAB25951	CNP analo	327	72	78.3	24	2	AAR40432	[D-Ala133
255	73	79.3	23	4	AAB91348	C-type na	328	72	78.3	25	2	AAR40431	[D-Ala133
256	73	79.3	27	2	AAR25950	CNP analo	329	72	78.3	25	2	AAR40429	[D-Ala133
257	73	79.3	27	2	AAR62358	Vasonatri	330	72	78.3	25	2	AAR40430	[D-Ala133
258	73	79.3	27	4	AAB91347	C-type na	331	72	78.3	25	2	AAR40430	[D-Ala133
259	73	79.3	27	8	ADL92008	Vasonatri	332	72	78.3	27	2	AAR11853	Bel natri
260	73	79.3	27	8	ADL91962	Vasonatri	333	72	78.3	27	4	AAB91306	Attrial-na
261	73	79.3	27	8	ADN03415	Exemplary	334	72	78.3	27	4	AAB91315	Attrial-na
262	73	79.3	27	8	ADR42250	Vasonatri	335	72	78.3	27	4	AAB91325	Attrial-na
263	73	79.3	28	2	AAR04811	Peptide a	336	72	78.3	32	2	AAB91325	Attrial-na
264	73	79.3	28	2	AAR93687	hANP(1-28	337	72	78.3	32	2	AAB91325	Attrial-na
265	73	79.3	28	2	AAR93099	Natriuret	338	72	78.3	32	3	AAW80235	Human B-t
266	73	79.3	28	6	ADA00776	Human hAN	339	72	78.3	32	3	AAW80235	Human B-t
267	73	79.3	29	2	AAR04817	Peptide w	340	72	78.3	32	3	AAW80246	Human B-t
268	73	79.3	29	2	AAR70094	Natriuret	341	71	77.2	37	4	AAR25986	Venticulu
269	73	79.3	29	4	AAB91289	Attrial-na	342	71	77.2	17	4	AAB91298	Attrial-na
270	73	79.3	29	4	AAB91238	Chicken b	343	71	77.2	17	5	ABG98263	Human C-t
271	73	79.3	29	9	ADV86895	NP peptid	344	71	77.2	17	5	ABG98266	Human C-t
272	73	79.3	30	3	AAW67297	Humah bra	345	71	77.2	18	2	AAR36963	ANVP #27
273	73	79.3	30	3	AAW51300	Humah B-t	346	71	77.2	18	2	AAR36963	ANVP #27
274	73	79.3	32	2	AAW51269	Human B-t	347	71	77.2	18	2	AAR40600	[Arg128] r
275	73	79.3	32	3	AAW80211	Human B-t	348	71	77.2	18	2	AAR40604	[Arg129] h
276	73	79.3	32	3	AAW80239	Human B-t	349	71	77.2	18	2	AAR40604	[Arg129] h
277	73	79.3	37	4	AB82544	Humah C-t	350	71	77.2	18	2	AAR40653	[D-Arg129
278	73	79.3	37	6	ABU63211	Chimeric	351	71	77.2	18	2	AAR40605	[Arg129] h
279	73	79.3	37	9	ADY62989	Natriuret	352	71	77.2	18	2	AAR40611	[Arg129] h
280	73	79.3	53	2	AAW16490	Human C-t	353	71	77.2	18	2	AAR40595	[Arg129] h
281	73	79.3	53	2	AAW21991	Porcine C	354	71	77.2	19	1	AAF80902	Human car
282	73	79.3	53	2	AD124859	C-type na	355	71	77.2	20	2	AAR40397	hANVP (127
283	73	79.3	53	4	AAB91344	C-type na	356	71	77.2	20	2	AAR40397	hANVP (127
284	73	79.3	53	4	AAB91343	C-type na	357	71	77.2	20	2	AAR36942	ANVP #6
285	73	79.3	53	8	ADL92007	C-type na	358	71	77.2	20	2	AAR40409	[D-Cys8130
286	73	79.3	103	3	AAW10489	Human pro	359	71	77.2	20	2	AAR40586	[Pro133] h
287	73	79.3	103	9	ADW46288	Sheep N-t	360	71	77.2	20	2	AAR40396	hANVP (127
288	73	79.3	103	9	ADW46287	Bovine N-	361	71	77.2	20	2	AAR40396	hANVP (127
289	73	79.3	103	9	ADW46291	Rat N-ter	362	71	77.2	20	1	AAR40480	[D-Cys8146
290	73	79.3	103	9	ADW46290	Mouse N-t	363	71	77.2	21	1	AAF71371	Antihyper
291	73	79.3	103	9	ADW46292	Pig N-ter	364	71	77.2	21	2	AAR40603	[Arg129] h
292	73	79.3	103	9	ADW46289	Human N-t	365	71	77.2	21	2	AAR40647	[Arg129] [
293	73	79.3	126	2	AAR29912	Humah CNP	366	71	77.2	21	2	AAR40610	[Arg129] [
294	73	79.3	126	2	AAR29913	Humah CNP	367	71	77.2	21	2	AAR40652	[D-Arg129
295	73	79.3	126	2	AAR20182	Sequence	368	71	77.2	22	1	AAF71374	Antihyper
296	73	79.3	126	2	AAR22188	Sequence	369	71	77.2	22	1	AAF71374	Antihyper
297	73	79.3	126	2	AAR22361	hCNP, 7/1	370	71	77.2	22	2	AAF82832	Human Atr
298	73	79.3	126	2	AAR20074	Sequence	371	71	77.2	22	2	AAR25705	Attrial na
299	73	79.3	126	2	AAW16491	Humah C-t	372	71	77.2	22	2	AAR25415	Attrial na
300	73	79.3	126	2	AAW21990	Porcine C	373	71	77.2	22	2	AAR29916	CNP analo
301	73	79.3	126	3	AAW10488	Humah pre	374	71	77.2	22	2	AAR29918	CNP analo
302	73	79.3	126	8	ABO84726	Humah can	375	71	77.2	22	2	AAR29917	CNP analo
303	73	79.3	126	8	ABO84725	Mouse can	376	71	77.2	22	2	AAR40602	[Arg129] h
304	73	79.3	126	8	ADW75286	Humah C-t	377	71	77.2	22	2	AAR40646	[Arg129] [
305	73	79.3	126	8	ADU05015	Amino aci	378	71	77.2	22	2	AAR40597	[Arg129] h
306	73	79.3	126	8	ADU04664	Humah C-t	379	71	77.2	22	2	AAR36961	ANVP #25
307	73	79.3	126	9	ADY34281	Humah c-t	380	71	77.2	22	2	AAR40598	[Arg129] h
308	73	79.3	152	8	AAR05669	Gamma-chi	381	71	77.2	22	4	AAW70089	Alpha hum
309	73	79.3	157	8	ADF86020	Truncated	382	71	77.2	22	4	AAW91299	Attrial-na
310	73	79.3	157	8	ADF86021	Truncated	383	71	77.2	22	4	AAE12433	Prog atri
311	72	78.3	17	5	ABG98247	Human C-t	384	71	77.2	22	8	ADL22348	Natriuret
312	72	78.3	17	5	ABG98248	Human C-t	385	71	77.2	22	8	ADL22347	Natriuret
313	72	78.3	17	5	ABG98242	Human C-t	386	71	77.2	23	9	ADV86890	Human alp
314	72	78.3	17	5	ABG98243	Human C-t	387	71	77.2	23	1	AAW82983	Alpha-hum
315	72	78.3	17	5	ABG98253	Human C-t	388	71	77.2	23	2	AAR25948	CNP analo
316	72	78.3	18	2	AAR40624	[Arg129] [389	71	77.2	23	2	AAR40609	[Arg129] [
												AAR40585	[Pro133] h

390	71	77.2	23	2	AAR40645	Aar40645 [Arg129] [463	71	77.2	28	1	AAP82005	Aap82005 Diuretic
391	71	77.2	23	2	AAR36976	Aar36976 ANVP #40.	464	71	77.2	28	1	AAP91314	Aap91314 Sequence
392	71	77.2	23	2	AAR36960	Aar36960 ANVP #24.	465	71	77.2	28	2	AAR03306	Aar03306 Human atr
393	71	77.2	23	2	AAR40395	Aar40395 hANVP (127	466	71	77.2	28	2	AAR04815	Aar04815 Peptide w
394	71	77.2	23	2	AAR40640	Aar40640 [Arg129] [467	71	77.2	28	2	AAR05859	Aar05859 Atrial na
395	71	77.2	23	2	AAR40394	Aar40394 hANVP (127	468	71	77.2	28	2	AAR03415	Aar03415 N-termina
396	71	77.2	23	2	AAR40479	Aar40479 D-Cys146	469	71	77.2	28	2	AAR29725	Aar29725 CNP analo
397	71	77.2	23	2	AAR40492	Aar40492 D-Ser148	470	71	77.2	28	2	AAR40042	Aar40042 Leu-(Gly)
398	71	77.2	23	2	AAR40596	Aar40596 [Arg129]h	471	71	77.2	28	2	AAR37109	Aar37109 Protected
399	71	77.2	23	2	AAR40651	Aar40651 D-Arg129	472	71	77.2	28	2	AAR37110	Aar37110 human atr
400	71	77.2	23	2	AAR40408	Aar40408 D-Cys130	473	71	77.2	28	2	AAR87093	Aar87093 Atrial na
401	71	77.2	23	2	AAR40608	Aar40608 [Arg128] [474	71	77.2	28	2	AAW11624	AAW11624 Target pe
402	71	77.2	23	2	AAR40505	Aar40505 D-Arg127	475	71	77.2	28	2	AAW70087	AAW70087 Alpha hum
403	71	77.2	23	2	AAR40593	Aar40593 [Arg139]r	476	71	77.2	28	2	AAW62656	AAW62656 Human atr
404	71	77.2	23	4	AAR91305	Aar91305 Atrial-na	477	71	77.2	28	2	AAW93094	AAW93094 Natriuret
405	71	77.2	24	2	AAR36940	Aar36940 ANVP #4.	478	71	77.2	28	3	AAW98488	AAW98488 pep 23 us
406	71	77.2	24	2	AAR40389	Aar40389 hANVP (127	479	71	77.2	28	3	AAW59033	AAW59033 Sequence
407	71	77.2	24	2	AAR40490	Aar40490 D-Ser148	480	71	77.2	28	3	AAO20102	AAO20102 Alpha-hum
408	71	77.2	24	2	AAR40390	Aar40390 hANVP (127	481	71	77.2	28	4	AAW82549	AAW82549 Human atr
409	71	77.2	24	2	AAR40478	Aar40478 D-Cys146	482	71	77.2	28	4	AAW45841	AAW45841 Nucleic a
410	71	77.2	24	2	AAR40503	Aar40503 D-Arg127	483	71	77.2	28	4	AAW81020	AAW81020 Atrial na
411	71	77.2	24	2	AAR40503	Aar40503 D-Cys129	484	71	77.2	28	4	AAW91319	AAW91319 Atrial-na
412	71	77.2	24	2	AAR40584	Aar40584 [Pro133]h	485	71	77.2	28	4	AAW91300	AAW91300 Atrial-na
413	71	77.2	24	2	AAR40406	Aar40406 D-Cys130	486	71	77.2	28	4	AAW45740	AAW45740 Human A-t
414	71	77.2	24	2	AAR40477	Aar40477 D-Cys146	487	71	77.2	28	4	AAU04278	AAU04278 Nuclear 1
415	71	77.2	24	2	AAR40407	Aar40407 D-Cys130	488	71	77.2	28	4	AAE12431	AAE12431 Human atr
416	71	77.2	24	2	AAR40491	Aar40491 D-Ser148	489	71	77.2	28	4	AAW70809	AAW70809 Human nat
417	71	77.2	24	2	AAR40504	Aar40504 D-Arg127	490	71	77.2	28	5	AAW80710	AAW80710 Human ANP
418	71	77.2	24	2	AAR40583	Aar40583 [Pro133]h	491	71	77.2	28	5	ABG98204	ABG98204 Human atr
419	71	77.2	24	4	AAW91297	Aaw91297 Atrial-na	492	71	77.2	28	6	ADA00783	ADA00783 Human nat
420	71	77.2	24	8	ADL22345	Adl22345 Natriuret	493	71	77.2	28	6	ADA00832	ADA00832 Human hAN
421	71	77.2	24	8	ADL22346	Adl22346 Natriuret	494	71	77.2	28	6	ADA00831	ADA00831 Human hAN
422	71	77.2	25	1	AAW51229	Aap51229 Sequence	495	71	77.2	28	6	ADA00829	ADA00829 Human hAN
423	71	77.2	25	1	AAW71467	Aap71467 Sequence	496	71	77.2	28	6	ADA00830	ADA00830 Human hAN
424	71	77.2	25	2	AAR40456	Aar40456 D-Leu143	497	71	77.2	28	6	ABU63214	ABU63214 Human atr
425	71	77.2	25	2	AAR40510	Aar40510 D-Ser129	498	71	77.2	28	7	ADP17067	ADP17067 Human alb
426	71	77.2	25	2	AAR40501	Aar40501 D-Arg127	499	71	77.2	28	8	ADL92004	ADL92004 Atrial na
427	71	77.2	25	2	AAR40509	Aar40509 D-Ser128	500	71	77.2	28	8	ADL22349	ADL22349 Natriuret
428	71	77.2	25	2	AAR40582	Aar40582 [Pro133]h	501	71	77.2	28	8	ADL22334	ADL22334 Natriuret
429	71	77.2	25	2	AAR40488	Aar40488 D-Ser148	502	71	77.2	28	8	ADL22331	ADL22331 Natriuret
430	71	77.2	25	2	AAR40508	Aar40508 D-Ser128	503	71	77.2	28	8	ADL22333	ADL22333 Natriuret
431	71	77.2	25	2	AAR40404	Aar40404 D-Cys130	504	71	77.2	28	8	ADL22330	ADL22330 Natriuret
432	71	77.2	25	2	AAR40441	Aar40441 D-Ala139	505	71	77.2	28	8	ADL22332	ADL22332 Natriuret
433	71	77.2	25	2	AAR40475	Aar40475 D-Cys146	506	71	77.2	28	8	ADM41340	ADM41340 Human atr
434	71	77.2	25	2	AAR40482	Aar40482 D-Adn147	507	71	77.2	28	8	ADN03290	ADN03290 Exemplary
435	71	77.2	25	2	AAR40388	Aar40388 hANVP (127	508	71	77.2	28	8	ADP18427	ADP18427 Neurogene
436	71	77.2	25	2	AAR40405	Aar40405 D-Cys130	509	71	77.2	28	8	ADP18427	ADP18427 Neurogene
437	71	77.2	25	2	AAR40489	Aar40489 D-Adn148	510	71	77.2	28	8	ADR42125	ADR42125 Atrial Na
438	71	77.2	25	2	AAR40494	Aar40494 D-Phe149	511	71	77.2	28	8	ADT92528	ADT92528 Cyclic pe
439	71	77.2	25	2	AAR40507	Aar40507 D-Ser127	512	71	77.2	28	9	ADW86888	ADW86888 Human alp
440	71	77.2	25	2	AAR40746	Aar40746 D-Arg136	513	71	77.2	28	9	ADW08063	ADW08063 Human bra
441	71	77.2	25	2	AAR36939	Aar36939 ANVP #3.	514	71	77.2	28	9	ADW5864	ADW5864 Human atr
442	71	77.2	25	2	AAR36955	Aar36955 ANVP #19.	515	71	77.2	28	9	ADW45305	ADW45305 Human fus
443	71	77.2	25	2	AAR40581	Aar40581 [Pro135]h	516	71	77.2	28	9	ADW62992	ADW62992 Human atr
444	71	77.2	25	2	AAR40744	Aar40744 D-Ile138	517	71	77.2	29	2	AAW13079	AAW13079 Tetradeca
445	71	77.2	25	2	AAR40748	Aar40748 D-Ala140	518	71	77.2	29	2	AAW13080	AAW13080 Tetradeca
446	71	77.2	25	2	AAR40476	Aar40476 D-Cys146	519	71	77.2	29	2	AAW67041	AAW67041 Atrial na
447	71	77.2	25	2	AAR40502	Aar40502 D-Arg127	520	71	77.2	29	8	ADL22335	ADL22335 Natriuret
448	71	77.2	25	2	AAR42954	Aar42954 Polypepti	521	71	77.2	31	4	AAW31170	AAW31170 Human PSA
449	71	77.2	25	4	AAW91304	Aaw91304 Atrial-na	522	71	77.2	31	4	AAW71941	AAW71941 Ubiquitin
450	71	77.2	25	8	ADL73465	Adl73465 Atrial na	523	71	77.2	32	1	AAW71466	AAW71466 Sequence
451	71	77.2	26	1	AAW50113	Aap50113 Biologica	524	71	77.2	32	1	AAW80388	AAW80388 Sequence
452	71	77.2	26	4	AAW91303	Aaw91303 Atrial-na	525	71	77.2	32	2	AAW88516	AAW88516 Uroiliati
453	71	77.2	27	2	AAW25949	Aar25949 CNP analo	526	71	77.2	32	2	AAW67039	AAW67039 Atrial na
454	71	77.2	28	1	AAW50048	Aap50048 Cardionat	527	71	77.2	32	2	AAW51279	AAW51279 Human B-t
455	71	77.2	28	1	AAW50172	Aap50172 Sequence	528	71	77.2	32	2	AAW51279	AAW51279 Human B-t
456	71	77.2	28	1	AAW50118	Aap50118 Sequence	529	71	77.2	32	2	AAW51277	AAW51277 Human B-t
457	71	77.2	28	1	AAW60076	Aap60076 Sequence	530	71	77.2	32	2	AAW51271	AAW51271 Human B-t
458	71	77.2	28	1	AAW61015	Aap61015 Alpha-fra	531	71	77.2	32	2	AAW51271	AAW51271 Human B-t
459	71	77.2	28	1	AAW61400	Aap61400 Alpha-hum	532	71	77.2	32	2	AAW51268	AAW51268 Human B-t
460	71	77.2	28	1	AAW71202	Aap71202 Lysine fr	533	71	77.2	32	2	AAW51268	AAW51268 Human B-t
461	71	77.2	28	1	AAW70655	Aap70655 Sequence	534	71	77.2	32	3	AAW80245	AAW80245 Human B-t
462	71	77.2	28	1	AAW71419	Aap71419 7,23-Cys (535	71	77.2	32	3	AAW80247	AAW80247 Human B-t

536	71	77.2	32	3	AAy80241	Humah B-t	609	70	76.1	22	2	AAr25956	AAr25956 CNP analo
537	71	77.2	32	3	AAy80238	Humah B-t	610	70	76.1	22	2	AAr29723	AAr29723 CNP analo
538	71	77.2	32	3	AAy80242	Human B-t	611	70	76.1	24	1	AAp94848	AAp94848 Sequence
539	71	77.2	32	3	AAy80244	Human B-t	612	70	76.1	25	2	AAr40710	[Lys133]r
540	71	77.2	32	3	AAy80249	Human B-t	613	70	76.1	28	6	ADA00828	Human hAN
541	71	77.2	32	4	AAb91328	Attrial-na	614	70	76.1	28	6	ADA00813	Human hAN
542	71	77.2	32	4	AAb70812	Humanuro	615	70	76.1	28	8	AdL22336	Natriuret
543	71	77.2	32	6	ADA00764	Human nat	616	69	75.0	17	2	AAW51310	Human B-t
544	71	77.2	32	7	AdF17063	Human alb	617	69	75.0	17	5	ABg98236	Human C-t
545	71	77.2	32	8	AdL22338	Natriuret	618	69	75.0	17	5	ABg98256	Human C-t
546	71	77.2	32	8	AdL22340	Natriuret	619	69	75.0	17	3	ABg98251	Human C-t
547	71	77.2	32	8	AdL22339	Natriuret	620	69	75.0	19	3	AAy80204	Human B-t
548	71	77.2	32	8	AdP49276	Natriuret	621	69	75.0	26	8	AdP49304	Natriuret
549	71	77.2	35	1	AAp50112	Biologica	622	69	75.0	28	6	ADA00824	Human hAN
550	71	77.2	35	1	AAp61765	Sequence	623	69	75.0	28	6	ADA00833	Human hAN
551	71	77.2	35	2	AAr08328	Chelated	624	69	75.0	28	6	ADA00814	Human hAN
552	71	77.2	35	2	AAr06353	Attrial na	625	69	75.0	28	6	ADA00826	Human hAN
553	71	77.2	40	2	AAw21945	Fusion pr	626	69	75.0	32	2	AAW51283	Human B-t
554	71	77.2	40	2	AAw33021	Fusion pr	627	69	75.0	32	2	AAW51280	Human B-t
555	71	77.2	42	2	AAr13323	Alpha-hum	628	69	75.0	32	3	AAy80250	Human B-t
556	71	77.2	43	1	AAp60078	Sequence	629	69	75.0	32	3	AAy80253	Human B-t
557	71	77.2	43	1	AAp81211	Alpha-hum	630	69	75.0	115	2	AAr29911	Type C na
558	71	77.2	56	4	AAb91313	Attrial-na	631	69	75.0	196	7	AdF44937	Heloderma
559	71	77.2	88	1	AAp50493	Cardiolil	632	69	75.0	265	6	ABp56118	Bothrops
560	71	77.2	101	9	AEb50531	Human hea	633	68	73.9	17	5	ABg98264	Human C-t
561	71	77.2	118	9	AEb50532	Human hea	634	68	73.9	17	5	ABg98271	Human C-t
562	71	77.2	125	1	AAp82656	Vasodilat	635	68	73.9	17	5	ABg98210	Human C-t
563	71	77.2	126	1	AAp50037	Sequence	636	68	73.9	17	5	ABg98249	Human C-t
564	71	77.2	126	1	AAp51240	Sequence	637	68	73.9	17	5	ABg98254	Human C-t
565	71	77.2	126	2	AAr00582	Humah gam	638	68	73.9	17	5	ABg98238	Human C-t
566	71	77.2	126	2	AAw34533	Humah atr	639	68	73.9	17	5	ABg98232	Human C-t
567	71	77.2	126	8	AdR75284	Humah atr	640	68	73.9	18	2	AAr40621	[Arg128]l
568	71	77.2	126	8	AdU005013	Amino aci	641	68	73.9	20	2	AAr40694	[Nle134]h
569	71	77.2	126	8	AdU04662	Humah atr	642	68	73.9	20	2	AAr40428	[D-Alal32
570	71	77.2	126	9	AdW95863	Humah pro	643	68	73.9	21	2	AAr40620	[Arg128]l
571	71	77.2	126	9	AdY34279	Humah atr	644	68	73.9	21	2	AAp50902	Sequence
572	71	77.2	128	8	AdP99246	Attrial na	645	68	73.9	22	1	AAr25708	Attrial na
573	71	77.2	129	3	AAb23976	Plasmid p	646	68	73.9	22	2	AAr29774	Attrial na
574	71	77.2	131	3	AAr13325	Cia prote	647	68	73.9	22	2	AAr29773	Attrial na
575	71	77.2	133	1	AAp60080	Sequence	648	68	73.9	22	4	AAE12441	Frog C-ty
576	71	77.2	136	2	AAr36935	Humah pre	649	68	73.9	23	2	AAr36975	ANVP #39.
577	71	77.2	144	2	AAr21677	Beta-gal	650	68	73.9	23	2	AAr36968	ANVP #32.
578	71	77.2	144	2	AAr21676	Beta-gal	651	68	73.9	23	2	AAr40427	[D-Alal32
579	71	77.2	147	2	AAr03301	Sequence	652	68	73.9	23	2	AAr40619	[Arg129]l
580	71	77.2	150	1	AAp51239	Sequence	653	68	73.9	23	2	AAr40695	[Nle134]h
581	71	77.2	150	1	AAp51241	Sequence	654	68	73.9	24	1	AAp50908	Sequence
582	71	77.2	151	1	AAp50050	Cardiolil	655	68	73.9	24	2	AAr40692	[Nle134]h
583	71	77.2	151	1	AAp50036	Sequence	656	68	73.9	24	2	AAr40693	[Nle134]h
584	71	77.2	151	1	AAp70629	Sequence	657	68	73.9	24	2	AAr40425	[D-Alal32
585	71	77.2	151	2	AAr36934	Humah pre	658	68	73.9	25	2	AAr36954	ANVP #18.
586	71	77.2	151	2	AAw98193	Humah atr	659	68	73.9	25	2	AAr40713	[Lys137]h
587	71	77.2	151	8	AdM41415	Humah atr	660	68	73.9	25	2	AAr40440	[D-Alal38
588	71	77.2	151	8	AdM41343	Humah pre	661	68	73.9	25	2	AAr40691	[Nle134]h
589	71	77.2	151	8	AdR75285	Humah atr	662	68	73.9	25	2	AAr36947	ANVP #11.
590	71	77.2	151	8	AdU05014	Amino aci	663	68	73.9	25	2	AAr40423	[D-Alal32
591	71	77.2	151	8	AdU04663	Humah atr	664	68	73.9	25	2	AAr36954	ANVP #18.
592	71	77.2	151	9	AdY34280	Humah atr	665	68	73.9	25	2	AAr40713	[Lys137]h
593	71	77.2	151	9	AEb50582	Humah atr	666	68	73.9	25	2	AAr40440	[D-Alal38
594	71	77.2	152	8	AdM41429	Bovine at	667	68	73.9	25	2	AAr40691	[Nle134]h
595	71	77.2	153	7	AdF44952	Human atr	668	68	73.9	25	2	AAr40690	[Nle134]h
596	71	77.2	161	5	ABP33228	Humah ORF	669	68	73.9	28	6	ADA00825	Human hAN
597	71	77.2	168	4	AAb81019	Inteleuk	670	68	73.9	28	8	AdL22342	Natriuret
598	71	77.2	198	5	ABp69270	Humah pol	671	68	73.9	28	6	AdL22342	Natriuret
599	71	77.2	240	2	AAr05425	Amino aci	672	68	73.9	32	3	AAW51278	Human B-t
600	71	77.2	241	1	AAp92070	Sequence	673	68	73.9	32	3	AAy80248	Human B-t
601	71	77.2	340	3	AAO20104	Gene-y al	674	67	72.8	17	1	AAp71036	Peptide w
602	71	77.2	637	9	AdW45218	Human ser	675	67	72.8	17	1	AAp71034	Peptide w
603	70	76.1	17	5	ABg98246	Human C-t	676	67	72.8	17	1	AAp82493	Cyclic pe
604	70	76.1	17	5	ABg98257	Human C-t	677	67	72.8	17	5	ABg98259	Human C-t
605	70	76.1	17	5	ABg98258	Human C-t	678	67	72.8	17	5	ABg98231	Human C-t
606	70	76.1	17	5	ABg98250	Human C-t	679	67	72.8	17	5	ABg98209	Human C-t
607	70	76.1	17	5	ABg98255	Human C-t	680	67	72.8	17	5	ABg98226	Human C-t
608	70	76.1	22	2	AAr25954	CNP analo	681	67	72.8	17	5	ABg98262	Human C-t

682	67	72.8	17	5	ABG98245	ABG98245 Human C-t	755	67	72.8	24	2	AAR36938	AAR36938 ANVP #2.
683	67	72.8	17	5	ABG98272	ABG98272 Human C-t	756	67	72.8	24	2	AAR40391	AAR40391 rANVP (126
684	67	72.8	17	5	ABG98227	ABG98227 Human C-t	757	67	72.8	24	2	AAR40577	AAR40577 [Pro132]r
685	67	72.8	17	5	ABG98229	ABG98229 Human C-t	758	67	72.8	24	2	AAR40471	AAR40471 [D-Cys145
686	67	72.8	17	5	ABG98237	ABG98237 Human C-t	759	67	72.8	24	2	AAR40498	AAR40498 [D-Arg126
687	67	72.8	17	5	ABG98230	ABG98230 Human C-t	760	67	72.8	24	2	AAR40402	AAR40402 [D-Cys129
688	67	72.8	17	6	AAR37839	AAR37839 Rat atria	761	67	72.8	24	2	AAR40497	AAR40497 [D-Arg126
689	67	72.8	18	2	AAR40601	AAR40601 [Arg128]r	762	67	72.8	24	4	AAB91311	AAB91311 Atrial-na
690	67	72.8	18	2	AAR40639	AAR40639 [Arg128]r	763	67	72.8	24	4	AAB91329	AAB91329 Atrial-na
691	67	72.8	18	2	AAR40650	AAR40650 [Pro132]r	764	67	72.8	24	4	AAB91326	AAB91326 Atrial-na
692	67	72.8	20	2	AAR40580	AAR40580 [Pro132]r	765	67	72.8	25	1	AAP51235	AAP51235 Sequence
693	67	72.8	20	2	AAR40474	AAR40474 [D-Cys145	766	67	72.8	25	1	AAP61016	AAP61016 Alpha-fra
694	67	72.8	20	2	AAR40403	AAR40403 [D-Cys129	767	67	72.8	25	1	AAP61025	AAP61025 Peptide h
695	67	72.8	20	2	AAR40500	AAR40500 [D-Arg126	768	67	72.8	25	2	AAR40741	AAR40741 [Glu136]h
696	67	72.8	20	2	AAR40393	AAR40393 rANVP (126	769	67	72.8	25	2	AAR36952	AAR36952 ANVP #16.
697	67	72.8	20	2	AAR40392	AAR40392 rANVP (126	770	67	72.8	25	2	AAR36956	AAR36956 ANVP #20.
698	67	72.8	21	1	AAP60769	AAP60769 Rat atrio	771	67	72.8	25	2	AAR40742	AAR40742 [D-Ile134
699	67	72.8	21	1	AAR36962	AAR36962 ANVP #26.	772	67	72.8	25	2	AAR36950	AAR36950 ANVP #14.
700	67	72.8	21	2	AAR40607	AAR40607 [Arg128]r	773	67	72.8	25	2	AAR36951	AAR36951 ANVP #15.
701	67	72.8	21	2	AAR40594	AAR40594 [Arg128]r	774	67	72.8	25	2	AAR36951	AAR36951 ANVP #15.
702	67	72.8	21	2	AAR40649	AAR40649 [D-Arg128	775	67	72.8	25	2	AAR40387	AAR40387 rANVP (126
703	67	72.8	21	2	AAR40638	AAR40638 [Arg128]r	776	67	72.8	25	2	AAR40443	AAR40443 [D-Ser141
704	67	72.8	21	4	AAB91307	AAB91307 Atrial-na	777	67	72.8	25	2	AAR36937	AAR36937 ANVP #1.
705	67	72.8	22	1	AAP50904	AAP50904 Sequence	778	67	72.8	25	2	AAR40410	AAR40410 [D-Phe130
706	67	72.8	22	1	AAP83168	AAP83168 Atrial Na	779	67	72.8	25	2	AAR40484	AAR40484 [D-Asn147
707	67	72.8	22	1	AAP83177	AAP83177 Atrial Na	780	67	72.8	25	2	AAR36944	AAR36944 ANVP #8.
708	67	72.8	22	2	AAR25713	AAR25713 Atrial na	781	67	72.8	25	2	AAR36945	AAR36945 ANVP #9.
709	67	72.8	22	2	AAR21589	AAR21589 ANF (7-28	782	67	72.8	25	2	AAR36953	AAR36953 ANVP #17.
710	67	72.8	22	2	AAR21588	AAR21588 ANF (7-28	783	67	72.8	25	2	AAR40745	AAR40745 [D-Asp135
711	67	72.8	22	2	AAR40644	AAR40644 [Arg128]r	784	67	72.8	25	2	AAR40398	AAR40398 [D-Cys129
712	67	72.8	22	2	AAR40592	AAR40592 [Arg128]r	785	67	72.8	25	2	AAR40399	AAR40399 [D-Cys129
713	67	72.8	22	2	AAR36959	AAR36959 ANVP #23.	786	67	72.8	25	2	AAR40576	AAR40576 [Pro132]r
714	67	72.8	22	8	ADL22343	ADL22343 Natriuret	787	67	72.8	25	2	AAR40743	AAR40743 [D-Ile137
715	67	72.8	22	8	ADL22353	ADL22353 Natriuret	788	67	72.8	25	2	AAR36946	AAR36946 ANVP #10.
716	67	72.8	22	8	ADL22344	ADL22344 Natriuret	789	67	72.8	25	2	AAR40470	AAR40470 [D-Cys145
717	67	72.8	23	1	AAP60770	AAP60770 Rat atrio	790	67	72.8	25	2	AAR40493	AAR40493 [D-Phe148
718	67	72.8	23	1	AAP71131	AAP71131 Sequence	791	67	72.8	25	2	AAR40495	AAR40495 [D-Arg126
719	67	72.8	23	1	AAP71148	AAP71148 Natriuret	792	67	72.8	25	2	AAR36948	AAR36948 ANVP #12.
720	67	72.8	23	1	AAP82915	AAP82915 4-fluoro-	793	67	72.8	25	2	AAR40481	AAR40481 [D-Asn146
721	67	72.8	23	1	AAP82984	AAP82984 Alpha-hum	794	67	72.8	25	2	AAR40483	AAR40483 [D-Asn147
722	67	72.8	23	2	AAR36941	AAR36941 ANVP #5.	795	67	72.8	25	2	AAR40496	AAR40496 [D-Arg126
723	67	72.8	23	2	AAR36969	AAR36969 ANVP #33.	796	67	72.8	25	4	AAB91312	AAB91312 Atrial-na
724	67	72.8	23	2	AAR36974	AAR36974 ANVP #38.	797	67	72.8	26	1	AAP51106	AAP51106 Sequence
725	67	72.8	23	2	AAR36974	AAR36974 ANVP #38.	798	67	72.8	26	1	AAP60807	AAP60807 Atrial na
726	67	72.8	23	2	AAR36967	AAR36967 ANVP #31.	799	67	72.8	26	1	AAP71130	AAP71130 Sequence
727	67	72.8	23	2	AAR40473	AAR40473 [D-Cys145	800	67	72.8	26	1	AAP70966	AAP70966 Sequence
728	67	72.8	23	2	AAR40499	AAR40499 [D-Arg126	801	67	72.8	26	2	AAR08309	AAR08309 Chelated
729	67	72.8	23	2	AAR36958	AAR36958 ANVP #22.	802	67	72.8	26	2	AAR21586	AAR21586 ANF (3-28
730	67	72.8	23	2	AAR36972	AAR36972 ANVP #36.	803	67	72.8	26	4	AAB91302	AAB91302 Atrial-na
731	67	72.8	23	2	AAR36971	AAR36971 ANVP #35.	804	67	72.8	27	1	AAP60084	AAP60084 Sequence
732	67	72.8	23	2	AAR40591	AAR40591 [Arg128]r	805	67	72.8	27	1	AAP71464	AAP71464 Sequence
733	67	72.8	23	2	AAR36977	AAR36977 ANVP #41.	806	67	72.8	27	1	AAP70970	AAP70970 Sequence
734	67	72.8	23	2	AAR40606	AAR40606 [Arg128]r	807	67	72.8	28	1	AAR03305	AAR03305 Rat atria
735	67	72.8	23	2	AAR40648	AAR40648 [D-Arg128	808	67	72.8	28	2	AAR04819	AAR04819 Peptide w
736	67	72.8	23	2	AAR36965	AAR36965 ANVP #29.	809	67	72.8	28	2	AAR04941	AAR04941 Atrial na
737	67	72.8	23	2	AAR36966	AAR36966 ANVP #30.	810	67	72.8	28	2	AAR03302	AAR03302 Sequence
738	67	72.8	23	2	AAR40599	AAR40599 [Arg128]r	811	67	72.8	28	2	AAR03302	AAR03302 Sequence
739	67	72.8	23	2	AAR40579	AAR40579 [Pro132]r	812	67	72.8	28	2	AAR03302	AAR03302 Sequence
740	67	72.8	23	2	AAR40637	AAR40637 [Arg128]r	813	67	72.8	28	2	AAR03302	AAR03302 Sequence
741	67	72.8	23	2	AAR40643	AAR40643 [Arg128]r	814	67	72.8	28	2	AAR03302	AAR03302 Sequence
742	67	72.8	23	2	AAR36973	AAR36973 ANVP #37.	815	67	72.8	28	3	AAB91310	AAB91310 Atrial-na
743	67	72.8	23	2	AAR40612	AAR40612 [Arg128]r	816	67	72.8	28	4	AAB91310	AAB91310 Atrial-na
744	67	72.8	23	2	AAR40612	AAR40612 [Arg128]r	817	67	72.8	28	4	AAB91310	AAB91310 Atrial-na
745	67	72.8	23	1	AAP50848	AAP50848 Sequence	818	67	72.8	28	6	ADA00771	ADA00771 Rat natri
746	67	72.8	24	1	AAP51230	AAP51230 Sequence	819	67	72.8	28	6	ADA00789	ADA00789 Human hAN
747	67	72.8	24	1	AAP60771	AAP60771 Rat atrio	820	67	72.8	28	6	ADA00785	ADA00785 Rat natri
748	67	72.8	24	1	AAP70964	AAP70964 Sequence	821	67	72.8	28	6	ADA00785	ADA00785 Rat natri
749	67	72.8	24	1	AAP94850	AAP94850 Sequence	822	67	72.8	28	9	ADQ26469	ADQ26469 Post-tran
750	67	72.8	24	2	AAR40485	AAR40485 [D-Asn147	823	67	72.8	31	1	AAP51105	AAP51105 Sequence
751	67	72.8	24	2	AAR40401	AAR40401 [D-Cys129	824	67	72.8	31	1	AAP71465	AAP71465 Sequence
752	67	72.8	24	2	AAR40486	AAR40486 [D-Asn147	825	67	72.8	32	1	AAP51104	AAP51104 Sequence
753	67	72.8	24	2	AAR40472	AAR40472 [D-Cys145	826	67	72.8	32	1	AAP51270	AAP51270 Human B-t
754	67	72.8	24	2	AAR40578	AAR40578 [Pro132]r	827	67	72.8	32	2	AAP51270	AAP51270 Human B-t

828	67	72.8	2	AAW51286	Aaw51286 Humah B-t	901	65	70.7	17	5	ABG98207	Abg98207 Human C-t
829	67	72.8	3	AAW80256	Aay80256 Humah B-t	902	65	70.7	17	5	ABG98265	Abg98265 Human C-t
830	67	72.8	32	AAW80240	Aay80240 Humah B-t	903	65	70.7	17	5	ABG98261	Abg98261 Human C-t
831	67	72.8	32	AAW91314	Aab91314 Atrial-na	904	65	70.7	17	5	ABG98235	Abg98235 Human C-t
832	67	72.8	33	AAW51103	Aap51103 Sequence	905	65	70.7	17	5	ABG98208	Abg98208 Human C-t
833	67	72.8	35	AAW60270	Aap60270 Sequence	906	65	70.7	18	2	AAR40630	Aar40630 [Arg129]
834	67	72.8	35	AAW08327	Aar08327 Chelated	907	65	70.7	18	2	AAR40618	Aar40618 [Arg129]
835	67	72.8	35	AAW06352	Aar06352 Atrial na	908	65	70.7	18	2	AAR40665	Aar40665 [Arg129]
836	67	72.8	48	AAW50115	Aap50115 Rat atria	909	65	70.7	18	2	AAR40636	Aar40636 [Arg129]
837	67	72.8	62	AAW60165	Aap60165 Rat recom	910	65	70.7	20	2	AAR40422	Aar40422 [D-Ala132]
838	67	72.8	71	AAW51102	Aap51102 Sequence	911	65	70.7	20	2	AAR40455	Aar40455 [D-Ala143]
839	67	72.8	73	AAW51107	Aap51107 Sequence	912	65	70.7	20	2	AAR40546	Aar40546 [D-Cys130]
840	67	72.8	111	AAW50565	Aap50565 Sequence	913	65	70.7	20	2	AAR40454	Aar40454 [D-Ala143]
841	67	72.8	126	AAW60017	Aap60017 Sequence	914	65	70.7	20	2	AAR40725	Aar40725 [Leu131]h
842	67	72.8	128	AAW51238	Aap51238 Sequence	915	65	70.7	20	2	AAR40534	Aar40534 [D-Ala132]
843	67	72.8	152	AAW51242	Aap51242 Sequence	916	65	70.7	20	2	AAR40468	Aar40468 [D-Ala145]
844	67	72.8	152	AAW60325	Aap60325 Ggamma-ra	917	65	70.7	20	2	AAR40707	Aar40707 [Ser136]h
845	67	72.8	152	AAW36936	Aar36936 Rat pre-p	918	65	70.7	21	2	AAR40629	Aar40629 [Arg129]
846	67	72.8	152	AAW98191	Aar98191 Rat atria	919	65	70.7	21	2	AAR40635	Aar40635 [Arg129]
847	67	72.8	152	AAW41352	Adm41352 Murine pr	920	65	70.7	21	2	AAR40664	Aar40664 [Arg129]
848	66	71.7	17	ABG98244	Abg98244 Human C-t	921	65	70.7	21	2	AAR40617	Aar40617 [Arg129]
849	66	71.7	17	ABG98234	Abg98234 Humah C-t	922	65	70.7	22	1	AAP71372	Aap71372 Antihyper
850	66	71.7	17	ABG98233	Abg98233 Humah C-t	923	65	70.7	22	2	AAR25711	Aar25711 Atrial na
851	66	71.7	20	AAW40568	Aar40568 [Asn136]h	924	65	70.7	22	2	AAR25712	Aar25712 Atrial na
852	66	71.7	20	AAW40574	Aar40574 [Phe134]r	925	65	70.7	22	2	AAR25743	Aar25743 Atrial na
853	66	71.7	20	AAW91293	Aab91293 Atrial-na	926	65	70.7	23	1	AAP71447	Aap71447 Natriuret
854	66	71.7	20	AAW05585	Abb05585 Dithiol p	927	65	70.7	23	1	AAP70962	Aap70962 Sequence
855	66	71.7	21	AAW03304	Aar03304 FANP-21 f	928	65	70.7	23	2	AAR40533	Aar40533 [D-Ala132]
856	66	71.7	21	AAW91294	Aab91294 Atrial-na	929	65	70.7	23	2	AAR40556	Aar40556 [D-Ala132]
857	66	71.7	22	AAW21828	Aar21828 Sequence	930	65	70.7	23	2	AAR40724	Aar40724 [Leu131]h
858	66	71.7	23	AAW82684	Alpha-hum	931	65	70.7	23	2	AAR40634	Aar40634 [Arg129]
859	66	71.7	23	AAW36978	Aar36978 ANVP #42.	932	65	70.7	23	2	AAR40663	Aar40663 [Arg129]
860	66	71.7	23	AAW40573	Aar40573 [Phe134]r	933	65	70.7	23	2	AAR40467	Aar40467 [D-Ala145]
861	66	71.7	23	AAW40567	Aar40567 [Asn136]h	934	65	70.7	23	2	AAR40545	Aar40545 [D-Cys130]
862	66	71.7	24	AAW03303	Aar03303 FANP-24 f	935	65	70.7	23	2	AAR40628	Aar40628 [Arg129]
863	66	71.7	24	AAW04818	Aar04818 Peptide w	936	65	70.7	23	2	AAR40421	Aar40421 [D-Ala132]
864	66	71.7	24	AAW04813	Aar04813 Peptide a	937	65	70.7	23	2	AAR40616	Aar40616 [Arg129]
865	66	71.7	24	AAW40565	Aar40565 [Asn136]h	938	65	70.7	23	2	AAR40706	Aar40706 [Ser136]h
866	66	71.7	24	AAW40566	Aar40566 [Asn136]h	939	65	70.7	23	2	AAR40552	Aar40552 [D-Ala132]
867	66	71.7	24	AAW40571	Aar40571 [Phe134]r	940	65	70.7	24	2	AAR04102	Aar04102 Intranasal
868	66	71.7	24	AAW40572	Aar40572 [Phe134]r	941	65	70.7	24	2	AAR40453	Aar40453 [D-Ala143]
869	66	71.7	24	AAW70091	Aaw70091 Atrial na	942	65	70.7	24	2	AAR40544	Aar40544 [D-Cys130]
870	66	71.7	24	AAW91295	Aab91295 Atrial-na	943	65	70.7	24	2	AAR40531	Aar40531 [D-Ala132]
871	66	71.7	24	AAW91292	Aab91292 Atrial-na	944	65	70.7	24	2	AAR40704	Aar40704 [Ser136]h
872	66	71.7	24	AAW12435	Aae12435 Frog atria	945	65	70.7	24	2	AAR40723	Aar40723 [Leu131]h
873	66	71.7	24	AAW86892	Adv86892 Bovine AN	946	65	70.7	24	2	AAR40452	Aar40452 [D-Ala143]
874	66	71.7	25	AAW51234	Aap51234 Sequence	947	65	70.7	24	2	AAR40532	Aar40532 [D-Ala132]
875	66	71.7	25	AAW40569	Aar40569 [Phe134]r	948	65	70.7	24	2	AAR40705	Aar40705 [Ser136]h
876	66	71.7	25	AAW40570	Aar40570 [Phe134]r	949	65	70.7	24	2	AAR40419	Aar40419 [D-Ala132]
877	66	71.7	25	AAW40564	Aar40564 [Asn136]h	950	65	70.7	24	2	AAR40465	Aar40465 [D-Ala145]
878	66	71.7	25	AAW40563	Aar40563 [Asn136]h	951	65	70.7	24	2	AAR40554	Aar40554 [D-Ala132]
879	66	71.7	25	AAW40575	Aar40575 [Pro132]r	952	65	70.7	24	2	AAR40420	Aar40420 [D-Ala132]
880	66	71.7	25	AAW40439	Aar40439 [D-Val137	953	65	70.7	24	2	AAR40543	Aar40543 [D-Cys130]
881	66	71.7	25	AAW36957	Aar36957 ANVP #21.	954	65	70.7	24	2	AAR40466	Aar40466 [D-Ala145]
882	66	71.7	26	AAW21585	Aar21585 ANF (3-28	955	65	70.7	24	2	AAR40722	Aar40722 [Leu131]h
883	66	71.7	28	AAW14469	Aar14469 Atrial na	956	65	70.7	24	2	AAR40555	Aar40555 [D-Ala132]
884	66	71.7	28	AAW93688	Aar93688 hANP(1-28	957	65	70.7	25	1	AAP51233	Aap51233 Sequence
885	66	71.7	28	AAW51309	Aaw51309 Humah A-t	958	65	70.7	25	2	AAR40530	Aar40530 [D-Ala132]
886	66	71.7	28	AAW93118	Aaw93118 Natriuret	959	65	70.7	25	2	AAR40451	Aar40451 [D-Ala143]
887	66	71.7	28	AAW93100	Aaw93100 Natriuret	960	65	70.7	25	2	AAR40590	Aar40590 [Ala132]h
888	66	71.7	28	AAW80217	Aay80217 Humah A-t	961	65	70.7	25	2	AAR40702	Aar40702 [Ser136]h
889	66	71.7	28	ADA00786	Ada00786 Humah hAN	962	65	70.7	25	2	AAR40720	Aar40720 [Leu131]h
890	66	71.7	28	ADA00768	Ada00768 Humah hAN	963	65	70.7	25	2	AAR40464	Aar40464 [D-Ala145]
891	66	71.7	30	AAW91296	Aab91296 Atrial-na	964	65	70.7	25	2	AAR40529	Aar40529 [D-Ala132]
892	66	71.7	32	AAW93690	Aar93690 Thr-Ala-p	965	65	70.7	25	2	AAR40535	Aar40535 [D-Cys129]
893	66	71.7	32	AAW51284	Aaw51284 Human beta-c	966	65	70.7	25	2	AAR40553	Aar40553 [D-Ala132]
894	66	71.7	32	AAW93102	Aaw93102 Natriuret	967	65	70.7	25	2	AAR40709	Aar40709 [Ile137]h
895	66	71.7	32	AAW80254	Aay80254 Human B-t	968	65	70.7	25	2	AAR40450	Aar40450 [D-Ala143]
896	66	71.7	32	ADA00767	Ada00767 Human hAN	969	65	70.7	25	2	AAR40418	Aar40418 [D-Ala132]
897	65.5	71.2	21	AAP71373	Aap71373 Antihyper	970	65	70.7	25	2	AAR40463	Aar40463 [D-Ala137]
898	65.5	71.2	24	AAW40436	Aar40436 [D-Met135	971	65	70.7	25	2	AAR40721	Aar40721 [Leu131]h
899	65.5	71.2	24	AAW40438	Aar40438 [D-Arg136	972	65	70.7	25	2	AAR40542	Aar40542 [D-Cys130]
900	65	70.7	17	AAW61004	Aap61004 Atrial na	973	65	70.7	25	2	AAR40703	Aar40703 [Ser136]h

974 65 70.7 25 2 AAR40541 [D-Cys]130
 975 65 70.7 25 2 AAR40417 [D-Ala]132
 976 65 70.7 25 2 AAR40523 [D-Ala]131
 977 65 70.7 25 2 AAR42955 Polypeptide
 978 65 70.7 26 1 AAR71129 Sequence
 979 65 70.7 28 1 AAR71696 Atrial na
 980 65 70.7 28 1 AAR71697 Atrial na
 981 65 70.7 28 6 ADA00821 Human hAN
 982 65 70.7 28 6 ADA00816 Human hAN
 983 65 70.7 28 8 ADL22337 Natriuret
 984 65 70.7 28 8 ADP49288 Natriuret
 985 65 70.7 29 2 AAR04814 Peptide a
 986 65 70.7 32 1 AAR71463 Sequence
 987 65 70.7 32 2 AAW51259 B-type na
 988 65 70.7 32 2 AAW51260 Type-B na
 989 65 70.7 32 3 AAY80207 Human B-t
 990 65 70.7 32 3 AAY80206 Human B-t
 991 65 70.7 35 1 AAR60806 Atrial na
 992 65 70.7 35 4 AAR91330 Atrial-na
 993 65 70.7 45 2 AAW51304 Mouse B-t
 994 65 70.7 45 3 AAY80224 Mouse B-t
 995 65 70.7 45 4 AAB91334 Brain nat
 996 65 70.7 116 1 AAP50102 Atrial na
 997 65 70.7 120 2 AAR54670 Mouse bra
 998 65 70.7 120 2 AAR54669 Mouse bra
 999 65 70.7 121 2 AAR54668 Mouse bra
 1000 65 70.7 121 2 AAR54667 Mouse bra

ALIGNMENTS

RESULT 1
 ADL22372
 ID ADL22372 standard; peptide; 17 AA.
 XX
 AC ADL22372;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Natriuretic peptide, SEQ ID NO 42.
 XX
 KW natriuretic peptide; NP; blood; cardiant; hypotensive; antiasthmatid;
 KW antiinflammatory; vasotropic; antilipaeic; nephrotropic;
 KW congestive heart failure; hypertension; asthma; inflammation;
 KW erectile dysfunction; hypercholesterolaemia; renal disorder.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..17
 FT Modified-site 17
 FT /note= "C-terminal amide"
 XX
 PN WO2004011498-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 29-JUL-2003; 2003WO-CA001097.
 XX
 PR 31-JUL-2002; 2002US-0400199P.
 PR 31-JUL-2002; 2002US-0400413P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Bakis P, Carrette J, Leclaire F, Leger R, Robitaille M;
 XX
 DR WPI; 2004-143823/14.
 XX
 PT New natriuretic peptide (NP) derivatives having a NP peptide and a
 PT reactive entity, useful for the treatment of congestive heart failure,
 PT hypertension, asthma, inflammation, hypercholesterolemia and renal
 disorders.

XX Claim 8; SEQ ID NO 42; 108pp; English.
 PS
 XX The invention relates to a novel long lasting natriuretic peptide (NP)
 XX derivative. The NP derivative comprises an NP peptide, having a 33 amino
 CC acid sequence, given in the specification, and a reactive entity coupled
 CC to the NP peptide, the reactive entity being capable of covalently
 CC bonding with a functionality on a blood component. The NP peptide has an
 CC extended in vivo half-life. The natriuretic peptide has the following
 CC activities: cardiant, hypotensive, antiasthmatid, antiinflammatory,
 CC vasotropic, antilipaeic, and nephrotropic. The methods and compositions
 CC of the present invention are useful for the treatment of congestive heart
 CC failure, hypertension, asthma, inflammation, erectile dysfunction,
 CC hypercholesterolaemia and renal disorders. This sequence represents a
 CC natriuretic peptide of the invention.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 92; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.5e-08; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 Db 1 CFGRKMDRISSSSGLGC 17
 RESULT 2
 ADL22373
 ID ADL22373 standard; peptide; 17 AA.
 XX
 AC ADL22373;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Natriuretic peptide, SEQ ID NO 43.
 XX
 KW natriuretic peptide; NP; blood; cardiant; hypotensive; antiasthmatid;
 KW antiinflammatory; vasotropic; antilipaeic; nephrotropic;
 KW congestive heart failure; hypertension; asthma; inflammation;
 KW erectile dysfunction; hypercholesterolaemia; renal disorder.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..17
 FT Modified-site 1
 FT /note= "Residue modified by MPA-AEEA"
 FT Modified-site 17
 FT /note= "C-terminal amide"
 XX
 PN WO2004011498-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 29-JUL-2003; 2003WO-CA001097.
 XX
 PR 31-JUL-2002; 2002US-0400199P.
 PR 31-JUL-2002; 2002US-0400413P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Bakis P, Carrette J, Leclaire F, Leger R, Robitaille M;
 XX
 DR WPI; 2004-143823/14.
 XX
 PT New natriuretic peptide (NP) derivatives having a NP peptide and a
 PT reactive entity, useful for the treatment of congestive heart failure,
 PT hypertension, asthma, inflammation, hypercholesterolemia and renal
 disorders.
 XX
 PS Claim 9; SEQ ID NO 43; 108pp; English.
 XX

CC The invention relates to a novel long lasting natriuretic peptide (NP)
 CC derivative. The NP derivative comprises an NP peptide, having a 33 amino
 CC acid sequence, given in the specification, and a reactive entity coupled
 CC to the NP peptide, the reactive entity being capable of covalently
 CC bonding with a functionality on a blood component. The NP peptide has an
 CC extended in vivo half-life. The natriuretic peptide has the following
 CC activities: cardiatic, hypotensive, antiasthmatic, antiinflammatory,
 CC vasotropic, antilipaeamic, and nephrotropic. The methods and compositions
 CC of the present invention are useful for the treatment of congestive heart
 CC failure, hypertension, asthma, inflammation, erectile dysfunction,
 CC hypercholesterolaemia and renal disorders. This sequence represents a
 CC natriuretic peptide of the invention.

XX Sequence 17 AA;
 SQ

Query Match 100.0%; Score 92; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.5e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 |||||
 DB 1 CFGRKMDRISSSSGLGC 17

RESULT 3
 AEB12959
 ID AEB12959 standard; peptide; 17 AA.
 XX
 AC AEB12959;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE Human brain natriuretic peptide, hBNP-32.

XX protein therapy; antibody engineering; hematopoiesis; immunotherapy;
 KW Cardiatic; Antidiabetic; Anorectic; cardiac failure; diabetes; obesity.
 XX
 OS Homo sapiens.

XX WO2005060642-A2.
 XX 07-JUL-2005.

XX 15-DEC-2004; 2004WO-US041946.
 XX 15-DEC-2003; 2003US-00737290.

XX (ALEX-) ALEXION PHARM INC.
 XX
 XX Bowdish KS, Frederickson S, Renshaw M, Orenica C;
 XX WPI; 2005-479402/48.

XX New immunoglobulin molecule comprising a region where amino acid residues
 XX corresponding to at least a portion of a complementarity determining
 XX region is replaced with a peptide, for treating congestive heart failure,
 XX diabetes, or obesity.

XX Disclosure; SEQ ID NO 172; 152pp; English.
 XX
 XX The invention relates to an immunoglobulin (Ig) molecule or its fragment
 XX comprising a region where amino acid residues corresponding to at least a
 XX portion of a complementarity determining regions (CDR) is replaced with a
 XX peptide selected from human brain natriuretic protein (hBNP), hBNP
 XX mimetics, glycogen phosphorylase (GLP)-1, GLP-1 mimetics, GLP-2, GLP-2
 XX mimetics, exendin, exendin mimetics, glucagons, glucagon mimetics and
 XX PACAP-38. Also included are a nucleic acid encoding the immunoglobulin
 XX molecule, an expression vector comprising the nucleic acid, a host cell
 XX transformed with the expression vector, producing the host cell under
 XX conditions suitable for expression of the immunoglobulin or its
 XX fragment), a composition comprising an immunoglobulin (or its fragment)
 XX and a pharmaceutically acceptable carrier, treating congestive heart

CC failure (comprising administering to the subject an immunoglobulin
 CC molecule or fragment comprising a region where amino acid residues
 CC corresponding to at least a portion of a CDR is replaced with a peptide
 CC selected from hBNP and hBNP mimetics), treating diabetes or obesity
 CC (comprising administering to a subject an immunoglobulin molecule or its
 CC fragment comprising a region where amino acid residues corresponding to
 CC at least a portion of a CDR is replaced with a peptide selected from GLP-
 CC 1, GLP-1 mimetics, GLP-2, GLP-2 mimetics, exendin, exendin mimetics,
 CC glucagons, glucagon mimetics and PACAP-38), preserving/improving beta-
 CC cell function (comprising administering to a subject an immunoglobulin
 CC molecule or fragment comprising a region where amino acid residues
 CC corresponding to at least a portion of a CDR is replaced with GLP-1),
 CC inducing endothelial-dependent relaxation of precontracted pulmonary
 CC artery rings (comprising administering to a subject an immunoglobulin
 CC molecule or fragment thereof comprising a region where amino acid
 CC residues corresponding to at least a portion of a CDR is replaced with
 CC GLP-1) and administering to a subject an immunoglobulin molecule or its
 CC fragment (comprising a region where amino acid residues corresponding to
 CC at least a portion of a complementarity determining regions (CDR) is
 CC replaced with a thiazolidinedione derivative), regulating adiponectin
 CC expression (comprising administering to a subject an immunoglobulin
 CC molecule or its fragment comprising a region where amino acid residues
 CC corresponding to at least a portion of a CDR is replaced with a
 CC thiazolidinedione derivative). The immunoglobulin is an anti-tetanus
 CC toxoid antibody (Tt) where the heavy chain CDR2 and/or CDR3 are fully or
 CC partially replaced with a peptide listed above or (as described in the
 CC examples) a Thrombopoietin (TPO) mimetic, erythropoietin (EPO) mimetic
 CC or ANP (atrial natriuretic peptide). The molecule, composition and
 CC methods are useful for treating congestive heart failure, diabetes or
 CC obesity. The present sequence is a peptide from the list above, for
 CC inclusion in an immunoglobulin of the invention.

XX Sequence 17 AA;
 SQ

Query Match 100.0%; Score 92; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.5e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 |||||
 DB 1 CFGRKMDRISSSSGLGC 17

RESULT 4
 ADL22374
 ID ADL22374 standard; peptide; 18 AA.

XX
 AC ADL22374;

XX 20-MAY-2004 (first entry)

XX Natriuretic peptide, SEQ ID No 44.

XX natriuretic peptide; NP; blood; cardiatic; hypotensive; antiasthmatic;
 KW antiinflammatory; vasotropic; antilipaeamic; nephrotropic;
 KW congestive heart failure; hypertension; asthma; inflammation;
 KW erectile dysfunction; hypercholesterolaemia; renal disorder.

XX Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1. .17
 FT Modified-site 18
 FT /note= "Residue modified by MPA-AEEA and C-terminal
 amide"

XX WO2004011498-A2.

XX 05-FEB-2004.

XX 29-JUL-2003; 2003WO-CA001097.

XX 31-JUL-2002; 2002US-0400199P.

PR 31-JUL-2002; 2002US-0400413P.
 XX (CONJ-) CONJUCHEM INC.
 XX
 PA Bridon DP, Bakis P, Carrette J, Leclaire F, Leger R, Robitaille M;
 XX WPI; 2004-143823/14.
 XX
 DR New natriuretic peptide (NP) derivatives having a NP peptide and a
 XX reactive entity, useful for the treatment of congestive heart failure,
 XX hypertension, asthma, inflammation, hypercholesterolemia and renal
 XX disorders.
 PT Claim 9; SEQ ID NO 44; 108pp; English.
 PS
 XX The invention relates to a novel long lasting natriuretic peptide (NP)
 XX derivative. The NP derivative comprises an NP peptide, having a 33 amino
 CC acid sequence, given in the specification, and a reactive entity coupled
 CC to the NP peptide, the reactive entity being capable of covalently
 CC bonding with a functionality on a blood component. The NP peptide has an
 CC extended in vivo half-life. The natriuretic peptide has the following
 CC activities: cardiant, hypotensive, antiasthmatic, antiinflammatory,
 CC vasotropic, antilipemic, and nephrotropic. The methods and compositions
 CC of the present invention are useful for the treatment of congestive heart
 CC failure, hypertension, asthma, inflammation, erectile dysfunction,
 CC hypercholesterolemia and renal disorders. This sequence represents a
 CC natriuretic peptide of the invention.
 XX Sequence 18 AA;
 SQ
 Query Match 100.0%; Score 92; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 DB 1 CFGRKMDRISSSSGLGC 17
 RESULT 5
 ADL22365
 ID ADL22365 standard; peptide; 23 AA.
 XX
 AC ADL22365;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Natriuretic peptide, SEQ ID No 35.
 XX
 KW natriuretic peptide; NP; blood; cardiant; hypotensive; antiasthmatic;
 KW antiinflammatory; vasotropic; antilipemic; nephrotropic;
 KW congestive heart failure; hypertension; asthma; inflammation;
 KW erectile dysfunction; hypercholesterolemia; renal disorder.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1. .17
 FT Modified-site 2 /note= "Residue modified by N-alpha-methyl"
 FT Modified-site 23 /note= "C-terminal amide"
 FT
 XX WO2004011498-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 29-JUL-2003; 2003WO-CA001097.
 XX
 XX 31-JUL-2002; 2002US-0400199P.
 PR 31-JUL-2002; 2002US-0400413P.
 XX
 PA (CONJ-) CONJUCHEM INC.

XX Bridon DP, Bakis P, Carrette J, Leclaire F, Leger R, Robitaille M;
 XX WPI; 2004-143823/14.
 XX
 DR New natriuretic peptide (NP) derivatives having a NP peptide and a
 XX reactive entity, useful for the treatment of congestive heart failure,
 XX hypertension, asthma, inflammation, hypercholesterolemia and renal
 XX disorders.
 PT Claim 9; SEQ ID NO 35; 108pp; English.
 PS
 XX The invention relates to a novel long lasting natriuretic peptide (NP)
 XX derivative. The NP derivative comprises an NP peptide, having a 33 amino
 CC acid sequence, given in the specification, and a reactive entity coupled
 CC to the NP peptide, the reactive entity being capable of covalently
 CC bonding with a functionality on a blood component. The NP peptide has an
 CC extended in vivo half-life. The natriuretic peptide has the following
 CC activities: cardiant, hypotensive, antiasthmatic, antiinflammatory,
 CC vasotropic, antilipemic, and nephrotropic. The methods and compositions
 CC of the present invention are useful for the treatment of congestive heart
 CC failure, hypertension, asthma, inflammation, erectile dysfunction,
 CC hypercholesterolemia and renal disorders. This sequence represents a
 CC natriuretic peptide of the invention.
 XX Sequence 23 AA;
 SQ
 Query Match 100.0%; Score 92; DB 8; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 DB 1 CFGRKMDRISSSSGLGC 17
 RESULT 6
 ADL22362
 ID ADL22362 standard; peptide; 23 AA.
 XX
 AC ADL22362;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Natriuretic peptide, SEQ ID No 32.
 XX
 KW natriuretic peptide; NP; blood; cardiant; hypotensive; antiasthmatic;
 KW antiinflammatory; vasotropic; antilipemic; nephrotropic;
 KW congestive heart failure; hypertension; asthma; inflammation;
 KW erectile dysfunction; hypercholesterolemia; renal disorder.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1. .17
 FT Modified-site 23 /note= "C-terminal amide"
 FT
 XX WO2004011498-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 29-JUL-2003; 2003WO-CA001097.
 XX
 XX 31-JUL-2002; 2002US-0400199P.
 PR 31-JUL-2002; 2002US-0400413P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 XX Bridon DP, Bakis P, Carrette J, Leclaire F, Leger R, Robitaille M;
 XX WPI; 2004-143823/14.
 XX

PT New natriuretic peptide (NP) derivatives having a NP peptide and a
PT reactive entity, useful for the treatment of congestive heart failure,
PT hypertension, asthma, inflammation, hypercholesterolemia and renal
PT disorders.
XX
XX Claim 9; SEQ ID NO 32; 108pp; English.
PS
CC The invention relates to a novel long lasting natriuretic peptide (NP)
CC derivative. The NP derivative comprises an NP peptide, having a 33 amino
CC acid sequence, given in the specification, and a reactive entity coupled
CC to the NP peptide, the reactive entity being capable of covalently
CC bonding with a functionality on a blood component. The NP peptide has an
CC extended in vivo half-life. The natriuretic peptide has the following
CC activities: cardiant, hypotensive, antiasthmatic, antiinflammatory,
CC vasotropic, antilipaeamic, and nephrotropic. The methods and compositions
CC of the present invention are useful for the treatment of congestive heart
CC failure, hypertension, asthma, inflammation, erectile dysfunction,
CC hypercholesterolaemia and renal disorders. This sequence represents a
CC natriuretic peptide of the invention.
XX
XX Sequence 23 AA;
SQ
Query Match 100.0%; Score 92; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. NO. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 1 CFGRKMDRISSSSGLGC 17

RESULT 7
ADL22364
ID ADL22364 standard; peptide; 23 AA.
XX
XX AC ADL22364;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Natriuretic peptide, SEQ ID NO 34.
XX
XX KW natriuretic peptide; NP; blood; cardiant; hypotensive; antiasthmatic;
XX antiinflammatory; vasotropic; antilipaeamic; nephrotropic;
XX congestive heart failure; hypertension; asthma; inflammation;
XX erectile dysfunction; hypercholesterolaemia; renal disorder.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 1..17
XX FT Modified-site 2 /note= "Residue modified by N-alpha-methyl"
XX FT Modified-site 23 /note= "C-terminal amide"
XX FT
XX WO2004011498-A2.
XX
XX PD 05-FEB-2004.
XX
XX PF 29-JUL-2003; 2003WO-CA001097.
XX
XX PR 31-JUL-2002; 2002US-0400199P.
XX PR 31-JUL-2002; 2002US-0400413P.
XX
XX PA (CONJ-) CONJUCHEM INC.
XX
XX PI Bridon DP, Bakis P, Carrette J, Leclaire F, Leger R, Robitaille M;
XX WPI; 2004-143823/14.
XX
XX PT New natriuretic peptide (NP) derivatives having a NP peptide and a
XX reactive entity, useful for the treatment of congestive heart failure,
XX hypertension, asthma, inflammation, hypercholesterolemia and renal
XX disorders.

PT disorders.
XX Claim 8; SEQ ID NO 34; 108pp; English.
XX
XX The invention relates to a novel long lasting natriuretic peptide (NP)
XX derivative. The NP derivative comprises an NP peptide, having a 33 amino
XX acid sequence, given in the specification, and a reactive entity coupled
XX to the NP peptide, the reactive entity being capable of covalently
XX bonding with a functionality on a blood component. The NP peptide has an
XX extended in vivo half-life. The natriuretic peptide has the following
XX activities: cardiant, hypotensive, antiasthmatic, antiinflammatory,
XX vasotropic, antilipaeamic, and nephrotropic. The methods and compositions
XX of the present invention are useful for the treatment of congestive heart
XX failure, hypertension, asthma, inflammation, erectile dysfunction,
XX hypercholesterolaemia and renal disorders. This sequence represents a
XX natriuretic peptide of the invention.
XX
XX Sequence 23 AA;
SQ
Query Match 100.0%; Score 92; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. NO. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 1 CFGRKMDRISSSSGLGC 17

RESULT 8
ADL22361
ID ADL22361 standard; peptide; 23 AA.
XX
XX AC ADL22361;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Natriuretic peptide, SEQ ID NO 31.
XX
XX KW natriuretic peptide; NP; blood; cardiant; hypotensive; antiasthmatic;
XX antiinflammatory; vasotropic; antilipaeamic; nephrotropic;
XX congestive heart failure; hypertension; asthma; inflammation;
XX erectile dysfunction; hypercholesterolaemia; renal disorder.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 1..17
XX FT Modified-site 23 /note= "C-terminal amide"
XX FT
XX WO2004011498-A2.
XX
XX PD 05-FEB-2004.
XX
XX PF 29-JUL-2003; 2003WO-CA001097.
XX
XX PR 31-JUL-2002; 2002US-0400199P.
XX PR 31-JUL-2002; 2002US-0400413P.
XX
XX PA (CONJ-) CONJUCHEM INC.
XX
XX PI Bridon DP, Bakis P, Carrette J, Leclaire F, Leger R, Robitaille M;
XX WPI; 2004-143823/14.
XX
XX PT New natriuretic peptide (NP) derivatives having a NP peptide and a
XX reactive entity, useful for the treatment of congestive heart failure,
XX hypertension, asthma, inflammation, hypercholesterolemia and renal
XX disorders.
XX
XX Claim 8; SEQ ID NO 31; 108pp; English.
XX
XX The invention relates to a novel long lasting natriuretic peptide (NP)

CC derivative. The NP derivative comprises an NP peptide, having a 33 amino
 CC acid sequence, given in the specification, and a reactive entity coupled
 CC to the NP peptide, the reactive entity being capable of covalently
 CC bonding with a functionality on a blood component. The NP peptide has an
 CC extended in vivo half-life. The natriuretic peptide has the following
 CC activities: cardiant, hypotensive, antiasthmatic, antiinflammatory,
 CC vasotropic, antilipemic, and nephrotropic. The methods and compositions
 CC of the present invention are useful for the treatment of congestive heart
 CC failure, hypertension, asthma, inflammation, erectile dysfunction,
 CC hypercholesterolaemia and renal disorders. This sequence represents a
 CC natriuretic peptide of the invention.

XX Sequence 23 AA;
 SQ Query Match 100.0%; Score 92; DB 8; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFGRKMDRISSSSGLGC 17
 Db 1 CFGRKMDRISSSSGLGC 17

RESULT 9
 AAB46799
 ID AAB46799 standard; peptide; 24 AA.

XX AAB46799;

XX 19-APR-2001 (first entry)

XX Human brain natriuretic peptide.

XX Brain natriuretic peptide; human; hypotensive; cardiant; hypertension;
 KW circulatory disease; edematous disease; cardiac failure; renal failure;
 KW smooth muscle relaxant.

XX Homo sapiens.

XX JP2000319299-A.

XX 21-NOV-2000.

XX 10-MAR-1989; 2000JP-00103212.

XX 10-MAR-1989; 99JP-00121666.

XX (SHIO) SHIONOGI & CO LTD.

XX (MATSU) MATSUO H.

XX WPI; 2001-184997/19.

XX New brain natriuretic peptide (BNP) having a cysteine bridge is useful for
 PT the treatment of circulatory diseases.

XX Claim 1; Page 2; 6pp; Japanese.

XX This invention describes a novel human brain natriuretic peptide (BNP)
 CC (I) having a cysteine bridge. The peptide of the invention has
 CC hypotensive, cardiant and smooth muscle relaxant activity. The peptide of
 CC the invention can be used for the treatment of circulatory diseases
 CC including hypertension, edematous diseases, and cardiac and renal failure

XX Sequence 24 AA;

XX Query Match 100.0%; Score 92; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFGRKMDRISSSSGLGC 17
 Db 2 CFGRKMDRISSSSGLGC 18

RESULT 10
 ADL22366
 ID ADL22366 standard; peptide; 24 AA.

XX ADL22366;

XX 20-MAY-2004 (first entry)

XX Natriuretic peptide, SEQ ID No 36.

XX natriuretic peptide; NP; blood; cardiant; hypotensive; antiasthmatic;
 KW antiinflammatory; vasotropic; antilipemic; nephrotropic;
 KW congestive heart failure; hypertension; asthma; inflammation;
 KW erectile dysfunction; hypercholesterolaemia; renal disorder.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1. 17

FT Modified-site 2 /note= "Residue modified by N-alpha-methyl"

FT Modified-site 24 /note= "Residue modified by MPA-AEEA and C-terminal
 FT amide"

XX WO2004011498-A2.

XX 05-FEB-2004.

XX 29-JUL-2003; 2003WO-CA001097.

XX 31-JUL-2002; 2002US-0400199P.

XX 31-JUL-2002; 2002US-0400413P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Bakis P, Carrette J, Leclaire F, Leger R, Robitaille M;

XX WPI; 2004-143823/14.

XX New natriuretic peptide (NP) derivatives having a NP peptide and a
 PT reactive entity, useful for the treatment of congestive heart failure,
 PT hypertension, asthma, inflammation, hypercholesterolemia and renal
 PT disorders.

XX Claim 9; SEQ ID NO 36; 108pp; English.

XX The invention relates to a novel long lasting natriuretic peptide (NP)
 CC derivative. The NP derivative comprises an NP peptide, having a 33 amino
 CC acid sequence, given in the specification, and a reactive entity coupled
 CC to the NP peptide, the reactive entity being capable of covalently
 CC bonding with a functionality on a blood component. The NP peptide has an
 CC extended in vivo half-life. The natriuretic peptide has the following
 CC activities: cardiant, hypotensive, antiasthmatic, antiinflammatory,
 CC vasotropic, antilipemic, and nephrotropic. The methods and compositions
 CC of the present invention are useful for the treatment of congestive heart
 CC failure, hypertension, asthma, inflammation, erectile dysfunction, a
 CC hypercholesterolaemia and renal disorders. This sequence represents a
 CC natriuretic peptide of the invention.

XX Sequence 24 AA;

XX Query Match 100.0%; Score 92; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFGRKMDRISSSSGLGC 17
 Db 1 CFGRKMDRISSSSGLGC 17

RESULT 11

ADL22363
 ID ADL22363 standard; peptide; 24 AA.
 XX AC ADL22363;
 XX DT 20-MAY-2004 (first entry)
 XX DE Natriuretic peptide, SEQ ID No 33.
 XX KW natriuretic peptide; NP; blood; cardiatic; hypotensive; antiasthmatic;
 XX KW antiinflammatory; vasotropic; antilipaeamic; nephrotropic;
 XX KW congestive heart failure; hypertension; asthma; inflammation;
 XX KW erectile dysfunction; hypercholesterolaemia; renal disorder.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Disulfide-bond 1. 17
 FT Modified-site 24 /note= "Residue modified by MPA-AEEA and C-terminal
 FT amide"
 XX WO2004011498-A2.
 XX 05-FEB-2004.
 XX 29-JUL-2003; 2003WO-CA001097.
 XX 31-JUL-2002; 2002US-0400199P.
 XX 31-JUL-2002; 2002US-0400413P.
 XX (CONJ-) CONJUCHEM INC.
 XX Bridon DP, Bakis P, Carrette J, Leclaire F, Leger R, Robitaille M;
 XX WPI; 2004-143823/14.
 XX New natriuretic peptide (NP) derivatives having a NP peptide and a
 PT reactive entity, useful for the treatment of congestive heart failure,
 PT hypertension, asthma, inflammation, hypercholesterolemia and renal
 PT disorders.
 XX Claim 9; SEQ ID NO 33; 108pp; English.
 XX The invention relates to a novel long lasting natriuretic peptide (NP)
 CC derivative. The NP derivative comprises an NP peptide, having a 33 amino
 CC acid sequence, given in the specification, and a reactive entity coupled
 CC to the NP peptide, the reactive entity being capable of covalently
 CC bonding with a functionality on a blood component. The NP peptide has an
 CC activities: cardiatic, hypotensive, antiasthmatic, antiinflammatory,
 CC vasotropic, antilipaeamic, and nephrotropic. The methods and compositions
 CC of the present invention are useful for the treatment of congestive heart
 CC failure, hypertension, asthma, inflammation, erectile dysfunction, a
 CC hypercholesterolaemia and renal disorders. This sequence represents a
 CC natriuretic peptide of the invention.
 XX Sequence 24 AA;
 SQ Query Match 100.0%; Score 92; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 DB 1 CFGRKMDRISSSSGLGC 17
 RESULT 12
 ADL22352
 ID ADL22352 standard; peptide; 25 AA.
 XX AC ADL22352;

XX 20-MAY-2004 (first entry)
 XX DE Natriuretic peptide, SEQ ID No 22.
 XX KW natriuretic peptide; NP; blood; cardiatic; hypotensive; antiasthmatic;
 XX KW antiinflammatory; vasotropic; antilipaeamic; nephrotropic;
 XX KW congestive heart failure; hypertension; asthma; inflammation;
 XX KW erectile dysfunction; hypercholesterolaemia; renal disorder.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Disulfide-bond 3. 19
 FT Modified-site 25 /note= "C-terminal amide"
 XX WO2004011498-A2.
 XX 05-FEB-2004.
 XX 29-JUL-2003; 2003WO-CA001097.
 XX 31-JUL-2002; 2002US-0400199P.
 XX 31-JUL-2002; 2002US-0400413P.
 XX (CONJ-) CONJUCHEM INC.
 XX Bridon DP, Bakis P, Carrette J, Leclaire F, Leger R, Robitaille M;
 XX WPI; 2004-143823/14.
 XX New natriuretic peptide (NP) derivatives having a NP peptide and a
 PT reactive entity, useful for the treatment of congestive heart failure,
 PT hypertension, asthma, inflammation, hypercholesterolemia and renal
 PT disorders.
 XX Claim 8; SEQ ID NO 22; 108pp; English.
 XX The invention relates to a novel long lasting natriuretic peptide (NP)
 CC derivative. The NP derivative comprises an NP peptide, having a 33 amino
 CC acid sequence, given in the specification, and a reactive entity coupled
 CC to the NP peptide, the reactive entity being capable of covalently
 CC bonding with a functionality on a blood component. The NP peptide has an
 CC activities: cardiatic, hypotensive, antiasthmatic, antiinflammatory,
 CC vasotropic, antilipaeamic, and nephrotropic. The methods and compositions
 CC of the present invention are useful for the treatment of congestive heart
 CC failure, hypertension, asthma, inflammation, erectile dysfunction, a
 CC hypercholesterolaemia and renal disorders. This sequence represents a
 CC natriuretic peptide of the invention.
 XX Sequence 25 AA;
 SQ Query Match 100.0%; Score 92; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 DB 3 CFGRKMDRISSSSGLGC 19
 RESULT 13
 AAY67295
 ID AAY67295 standard; peptide; 26 AA.
 XX AC AAY67295;
 XX 05-APR-2000 (first entry)
 XX DE Human brain natriuretic peptide (BNP) fragment 1.
 XX

KW Brain natriuretic peptide; BNP; smooth muscle relaxant; hypertension;
 KW sodium diuretic activity; congestive heart failure; renal failure;
 KW oedema.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..3
 FT /note= "Optionally replaced by a Hydrogen atom"
 FT Disulfide-bond 4..20
 XX
 XX JP11343299-A.
 XX
 XX 14-DEC-1999.
 XX
 XX 10-MAR-1989; 99JP-00121666.
 XX
 XX 10-MAR-1989; 98JP-00131506.
 XX (SHIO) SHIONOGI & CO LTD.
 XX (MATS/) MATSUO T.
 XX
 DR WPI; 2000-102193/09.
 XX
 XX New peptides are smooth muscle relaxants and sodium diuretics - used to
 PT treat cardiac, renal, hepatic and pulmonary edema, hypertension,
 PT congestive heart failure, renal failure and hypertension.
 XX
 PS Claim 1; Page 2; 5pp; Japanese.
 XX
 XX This is a human brain natriuretic peptide (BNP) sequence. The peptide is
 CC a safe smooth muscle relaxant with sodium diuretic activity. The peptide
 CC can be used in the treatment of cardiac, renal, hepatic and pulmonary
 CC oedema, hypertension, congestive heart failure and acute and chronic
 CC renal failure
 XX
 XX Sequence 26 AA;
 SQ
 Query Match 100.0%; Score 92; DB 3; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 Db 4 CFGRKMDRISSSSGLGC 20
 RESULT 14
 ID ABU63216
 ABU63216 standard; peptide; 26 AA.
 AC
 AC ABU63216;
 XX
 XX 15-OCT-2003 (first entry)
 DT
 XX N-terminus of human brain natriuretic peptide (BNP).
 DE
 XX Natriuretic; renin-suppressing; diuretic; vasodilator; heart failure;
 KW cardiovascular disorder; congestive heart failure; hypertension;
 KW acute kidney failure; chronic kidney failure; liver cirrhosis;
 KW nephrotic syndrome; oedematous state; cardiant; BNP; human;
 KW brain natriuretic peptide.
 XX
 XX Homo sapiens.
 OS
 XX US2003069186-A1.
 PN
 XX 10-APR-2003.
 PD
 XX 26-MAR-2002; 2002US-00106806.
 PF
 XX 17-DEC-1999; 99US-00466268.
 PR
 XX

PA (BURN/) BURNETT J C.
 PA (LISY/) LISY O.
 XX
 PI Burnett JC, Lisy O;
 XX
 XX WPI; 2003-576433/54.
 DR
 XX Novel peptide compound useful for treating or preventing cardiovascular
 XX disorders e.g. congestive heart failure, has natriuretic, renin-
 PT suppressing, diuretic and/or vasodilator activity in mammals.
 PT
 XX Claim 4; Page 2; 43pp; English.
 PS
 XX The present invention relates to chimeric peptides having natriuretic,
 CC renin-suppressing, diuretic and/or vasodilator activity in mammals. The
 CC peptides of the invention are useful for treating heart failure in a
 CC mammal e.g. human, rat, mouse, canine, bovine, equine, ovine, caprine or
 CC feline. They are useful for treating and preventing cardiovascular
 CC disorders e.g. congestive heart failure, acute or chronic kidney failure,
 CC hypertension, cirrhosis of liver, nephrotic syndrome and other oedematous
 CC states. The present sequence represents the N-terminus of human brain
 CC natriuretic peptide (BNP)
 XX
 XX Sequence 26 AA;
 SQ
 Query Match 100.0%; Score 92; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 Db 10 CFGRKMDRISSSSGLGC 26
 RESULT 15
 ADL22354
 ID ADL22354 standard; peptide; 26 AA.
 XX
 XX AC ADL22354;
 XX
 XX 20-MAY-2004 (first entry)
 DT
 XX Natriuretic peptide, SEQ ID No 24.
 DE
 XX natriuretic peptide; NP; blood; cardiant; hypotensive; antiasthmatic;
 KW antiinflammatory; vasotropic; antilipaeamic; nephrotropic;
 KW congestive heart failure; hypertension; asthma; inflammation;
 KW erectile dysfunction; hypercholesterolaemia; renal disorder.
 XX
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 3..19
 FT Modified-site 26
 FT /note= "Residue modified by MPA-AEEA and C-terminal
 FT amide"
 FT
 FT WO2004011498-A2.
 XX
 XX 05-FEB-2004.
 PD
 XX 29-JUL-2003; 2003WO-CA001097.
 PF
 XX 31-JUL-2002; 2002US-0400199P.
 XX
 XX 31-JUL-2002; 2002US-0400413P.
 PR
 XX (CONJ-) CONJUCHEM INC.
 PA
 XX Bridon DP, Bakis P, Carrette J, Leclaire P, Leger R, Robitaille M;
 PI
 XX WPI; 2004-143823/14.
 DR
 XX New natriuretic peptide (NP) derivatives having a NP peptide and a
 PT

PT reactive entity, useful for the treatment of congestive heart failure,
 PT hypertension, asthma, inflammation, hypercholesterolemia and renal
 PT disorders.

PS Claim 9; SEQ ID NO 24; 108pp; English.

XX The invention relates to a novel long lasting natriuretic peptide (NP)
 XX derivative. The NP derivative comprises an NP peptide, having a 33 amino
 CC acid sequence, given in the specification, and a reactive entity coupled
 CC to the NP peptide, the reactive entity being capable of covalently
 CC bonding with a functionality on a blood component. The NP peptide has an
 CC extended in vivo half-life. The natriuretic peptide has the following
 CC activities: cardiant, hypotensive, antiasthmatic, antiinflammatory,
 CC vasotropic, antilipemic, and nephrotropic. The methods and compositions
 CC of the present invention are useful for the treatment of congestive heart
 CC failure, hypertension, asthma, inflammation, erectile dysfunction,
 CC hypercholesterolemia and renal disorders. This sequence represents a
 CC natriuretic peptide of the invention.

XX Sequence 26 AA;

Query Match 100.0%; Score 92; DB 8; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 |||||
 Db 3 CFGRKMDRISSSSGLGC 19

RESULT 16

ADP49303
 ID ADP49303 standard; peptide; 26 AA.

AC ADP49303;

DT 26-AUG-2004 (first entry)

DE Natriuretic compound polypeptide #46.

KW cardiant; hypotensive; natriuretic compound; heart failure; hypertension;
 KW extracellular fluid.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 3 /note= "Xaa-any amino acid except Lys"

PN WO2004047871-A2.

XX 10-JUN-2004.

XX 12-NOV-2003; 2003WO-US037996.

XX 26-NOV-2002; 2002US-0429151P.

XX (NOBE-) NOBEX CORP.

PI James KD, Radhakrishnan B, Malkar NB, Miller MA, Ekwuribe NN;

DR WPI; 2004-450218/42.

XX Natriuretic compound conjugate useful in the treatment of e.g. congestive
 PT heart failure, comprises natriuretic compound and at least one modifying
 PT moiety.

PS Example 25; Page 77; 125pp; English.

XX The present invention relates to a natriuretic compound, which comprises
 CC a natriuretic compound containing a natriuretic molecule NPR-A
 CC (natriuretic peptide receptor-A) binding site and at least one modifying
 CC moiety conjugation site, and at least one modifying moiety attached to

CC the modifying moiety conjugation site. The conjugates are used for the
 CC treatment of a condition involving an excess level of extracellular fluid
 CC e.g. chronic or acute congestive heart failure and hypertension. The
 CC present sequence is a peptide shown in the invention.

XX Sequence 26 AA;

Query Match 100.0%; Score 92; DB 8; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 |||||
 Db 10 CFGRKMDRISSSSGLGC 26

RESULT 17

ADP49273

ID ADP49273 standard; peptide; 26 AA.

AC ADP49273;

DT 26-AUG-2004 (first entry)

DE Natriuretic compound polypeptide #16.

KW cardiant; hypotensive; natriuretic compound; heart failure; hypertension;
 KW extracellular fluid.

OS Synthetic.

PN WO2004047871-A2.

XX 10-JUN-2004.

XX 12-NOV-2003; 2003WO-US037996.

XX 26-NOV-2002; 2002US-0429151P.

XX (NOBE-) NOBEX CORP.

PI James KD, Radhakrishnan B, Malkar NB, Miller MA, Ekwuribe NN;

DR WPI; 2004-450218/42.

XX Natriuretic compound conjugate useful in the treatment of e.g. congestive
 PT heart failure, comprises natriuretic compound and at least one modifying
 PT moiety.

PS Claim 18; Page 93; 125pp; English.

XX The present invention relates to a natriuretic compound, which comprises
 CC a natriuretic compound containing a natriuretic molecule NPR-A
 CC (natriuretic peptide receptor-A) binding site and at least one modifying
 CC moiety conjugation site, and at least one modifying moiety attached to
 CC the modifying moiety conjugation site. The conjugates are used for the
 CC treatment of a condition involving an excess level of extracellular fluid
 CC e.g. chronic or acute congestive heart failure and hypertension. The
 CC present sequence is a peptide shown in the invention.

XX Sequence 26 AA;

Query Match 100.0%; Score 92; DB 8; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 |||||
 Db 10 CFGRKMDRISSSSGLGC 26

RESULT 18

ADW45317

ID ADW45317 standard; peptide; 26 AA.
XX AC ADW45317;
XX DT 07-APR-2005 (first entry)
XX DE Human fusion-related BNP (brain natriuretic peptide) peptide - SEQ 321.
XX KW fusion protein; anti-HIV; gastrointestinal-gen.; antidiabetic; anorectic;
KW nephrotropic; cardiant; cytostatic; neuroprotective; immunosuppressive;
KW immune disorder; hematological disease; hyperproliferative disorder;
KW renal disease; cardiovascular disease; cardiovascular-gen.;
KW respiratory disorder; angiogenesis disorder; neurological disease;
KW wound healing; vulnary; endocrine disease; reproductive disorder;
KW gynecological; infectious disease; antimicrobial;
KW gastrointestinal disease; gene therapy; BNP; brain natriuretic peptide.
XX KW Homo sapiens.
XX OS WO2005003296-A2.
XX FN 13-JAN-2005.
XX PD 20-JAN-2004; 2004WO-US001369.
XX PF 22-JAN-2003; 2003US-0441305P.
XX PR 11-MAR-2003; 2003US-0453201P.
XX PR 02-MAY-2003; 2003US-0467222P.
XX PR 23-MAY-2003; 2003US-0472816P.
XX PR 06-JUN-2003; 2003US-0476267P.
XX PR 24-SEP-2003; 2003US-0505172P.
XX PR 30-SEP-2003; 2003US-0506746P.
XX KW (HUMA-) HUMAN GENOME SCI INC.
XX PI Haseltine WA, Rosen CA;
XX WPI; 2005-091786/10.
XX N-PSDB; ADW45143.
XX KW New albumin fusion protein for diagnosing, treating or preventing
PT diseases such as HIV/AIDS, diabetes, obesity, heart disease or immune
PT disorders comprises a therapeutic protein (e.g. CD4W33, GUP-2 or PACAP-
PT 27) and an albumin.
XX Example 4; SEQ ID NO 321; 884pp; English.
XX CC The invention relates to a novel albumin fusion protein comprising a
CC therapeutic protein as listed in the specification in Table 1 and an
CC albumin comprising a sequence of SEQ ID NO: 1, or a fragment or variant
CC of SEQ ID NO: 1, where the fragment or variant has albumin activity and
CC where the albumin activity is the ability to prolong the shelf life of
CC the therapeutic protein compared to the shelf-life of the therapeutic
CC protein in an unfused state. Human serum albumin (HSA, HA) is responsible
CC for a significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion
CC protein of the invention demonstrates anti-HIV, gastrointestinal-gen.,
CC antidiabetic, anorectic, cardiant and immunosuppressive activities. The
CC fusion protein may be useful for diagnosing, treating, preventing or
CC ameliorating diseases, such as immune disorders, blood disorders
CC hyperproliferative disorders, renal disorders, cardiovascular disorders,
CC respiratory disorders, angiogenesis-related disorders, neurological
CC disorders, wound healing disorders, endocrine disorders, reproductive
CC disorders, infectious disorders and gastrointestinal disorders, possibly
CC with the use of gene therapy techniques. The current sequence is that of
CC the human fusion-related BNP (brain natriuretic peptide) peptide - SEQ
CC 321 of the invention.
XX SQ Sequence 26 AA;

Query Match 100.0%; Score 92; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CFGRMDRISSSSGLGC 17
DB 10 CFGRMDRISSSSGLGC 26
RESULT 19
ADY62994
ID ADY62994 standard; peptide; 26 AA.
XX AC ADY62994;
XX DT 02-JUN-2005 (first entry)
XX DE Human brain natriuretic peptide (BNP) N-terminus SEQ ID NO:7.
XX KW natriuretic peptide; diuretic peptide; vasodilator; cardiant;
KW nephrotropic; hypotensive; hepatotropic; antiinflammatory;
KW cardiac failure; renal failure; hypertension; liver cirrhosis;
KW nephrotic syndrome; edema; cardiovascular disease.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Disulfide-bond 10. .26
XX PN US2005059600-A1.
XX PD 17-MAR-2005.
XX PF 23-SEP-2004; 2004US-00947730.
XX PR 17-DEC-1999; 99US-00466268.
XX PR 26-MAR-2002; 2002US-00106806.
XX KW (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX PI Burnett JC, Lisy O;
XX WPI; 2005-222252/23.
XX KW New peptides of Dendroaspis with vasodilatory, natriuretic, diuretic or
PT renin suppression activity useful to treat heart failure, congestive
PT heart failure, acute or chronic kidney failure, hypertension, cirrhosis
PT and nephrotic syndrome.
XX PS Claim 4; SEQ ID NO 7; 43pp; English.
XX CC The invention relates to peptides (I) of Dendroaspis of formula X0-Pro-X1
CC -A5-Al-A3-Pro-Al-Pro-Al-A5-Pro-X1-X1-X1-A4. Where A1 is Leu, Lys, Arg,
CC His, Orn, Asn or Gln; A3 is Asp or Glu; A4 is Lys, Arg, Orn, Ala, Thr,
CC Asn or Gln; A5 is Gly, Ala, Val, Met, Leu, Norleucine or Ile; X1 Ser or
CC Thr; and X0 is absent or is a 1-35 amino acid peptide, provided that X0
CC is not Glu-Val-Lys-Tyr-Asp-Pro-Cys-Phe-Gly-His-Lys-Ile-Asp-Arg-Ile-Asn-
CC His-Val-Ser-Asn-Leu-Gly-Cys (ADY62998); and (I) is not the 41 amino acid
CC sequence of ADY62988. Also described: (1) a compound (II) comprising a
CC variant of the 15 amino acid sequence of ADY62990, where the variant has
CC one or more amino acid substitutions of Pro to Gly; Ser to Thr; Thr to
CC Ser; Arg to Lys; Gln or Asn; Ala to Val, Ile, or Leu; Leu to Nor, Ile,
CC Val, Met, Ala or Phe; Asp to Glu; and Asn to Gln, His, Lys or Arg; and
CC (2) a composition useful as a natriuretic, diuretic, renin suppressor or
CC vasodilator comprising (I) or (II) with a pharmaceutically acceptable
CC carrier. (I) and (II) are useful in the treatment of heart failure in a
CC mammal such as human, rat, mouse, canine, bovine, equine, ovine, caprine
CC or feline. (I) either singly or in combination can be used to treat,
CC ameliorate or prevent congestive heart failure, acute or chronic kidney
CC failure, hypertension, cirrhosis of the liver, nephrotic syndrome and
CC other edematous states. The ability of (I) to treat heart failure was
CC tested in seven male mongrel dogs. The results showed that (I) potently
CC possessed renin-suppressing action. The present sequence represents the N
CC -terminus of human brain natriuretic peptide (BNP) from the present
CC invention.

```

XX SQ Sequence 26 AA;
Query Match 100.0%; Score 92; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSGLGC 17
Db 10 CFCGRKMDRISSSSGLGC 26

RESULT 20
ADP49289
ID ADP49289 standard; peptide; 27 AA.
XX AC ADP49289;
XX DT 26-AUG-2004 (first entry)
XX XX Natriuretic compound polypeptide #32.
DE DE cardiant; hypotensive; natriuretic compound; heart failure; hypertension;
XX extracellular fluid.
XX OS Synthetic.
XX XX Key Location/Qualifiers
FH Misc-difference 27
FT FT /note= "Xaa=1 to 10 amino acid"
XX WO2004047871-A2.
XX PD 10-JUN-2004.
XX PF 12-NOV-2003; 2003WO-US037996.
XX XX 26-NOV-2002; 2002US-0429151P.
XX PA (NOBE-) NOBEX CORP.
XX PI James KD, Radhakrishnan B, Malkar NB, Miller MA, Ekwuribe NN;
XX DR WPI; 2004-450218/42.
XX XX Natriuretic compound conjugate useful in the treatment of e.g. congestive
PT heart failure, comprises natriuretic compound and at least one modifying
PT moiety.
XX PS Example 25; Page 76; 125pp; English.
XX CC The present invention relates to a natriuretic compound, which comprises
CC a natriuretic compound containing a natriuretic molecule NPR-A
CC (natriuretic peptide receptor-A) binding site and at least one modifying
CC moiety conjugation site, and at least one modifying moiety attached to
CC the modifying moiety conjugation site. The conjugates are used for the
CC treatment of a condition involving an excess level of extracellular fluid
CC e.g. chronic or acute congestive heart failure and hypertension. The
CC present sequence is a peptide shown in the invention.
XX XX Sequence 27 AA;
Query Match 100.0%; Score 92; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSGLGC 17
Db 10 CFCGRKMDRISSSSGLGC 26

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RESULT 21
ADW45318

```

ID ADW45318 standard; peptide; 27 AA.
XX AC ADW45318;
XX DT 07-APR-2005 (first entry)
XX DE Human fusion-related BNP (brain natriuretic peptide) peptide - SEQ 322.
XX XX fusion protein; anti-HIV; gastrointestinal-gen.; antidiabetic; anorectic;
KW nephrotropic; cardiant; cytostatic; neuroprotective; immunosuppressive;
KW immune disorder; hematological disease; hyperproliferative disorder;
KW renal disease; cardiovascular disease; cardiovascular-gen.;
KW respiratory disorder; angiogenesis disorder; neurological disease;
KW wound healing; vulnery; endocrine disease; reproductive disorder;
KW gynecological; infectious disease; antimicrobial;
KW gastrointestinal disease; gene therapy; BNP; brain natriuretic peptide.
XX OS Homo sapiens.
XX XX WO2005003296-A2.
XX PD 13-JAN-2005.
XX PF 20-JAN-2004; 2004WO-US001369.
XX XX 22-JAN-2003; 2003US-0441305P.
PR 11-MAR-2003; 2003US-0453201P.
PR 02-MAY-2003; 2003US-0467222P.
PR 23-MAY-2003; 2003US-0472816P.
PR 06-JUN-2003; 2003US-0476267P.
PR 24-SEP-2003; 2003US-0505172P.
PR 30-SEP-2003; 2003US-0506746P.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PI Haseltine WA, Rosen CA;
XX XX WPI; 2005-091786/10.
DR DR N-PSDB; ADW45144.
XX XX New albumin fusion protein for diagnosing, treating or preventing
PT diseases such as HIV/AIDS, diabetes, obesity, heart disease or immune
PT disorders comprises a therapeutic protein (e.g. CD4M33, GLP-2 or PACAP-
PT 27) and an albumin.
XX PS Example 4; SEQ ID NO 322; 884pp; English.
XX CC The invention relates to a novel albumin fusion protein comprising a
CC therapeutic protein as listed in the specification in Table 1 and an
CC albumin comprising a sequence of SEQ ID NO: 1, or a fragment or variant
CC of SEQ ID NO: 1, where the fragment or variant has albumin activity and
CC where the albumin activity is the ability to prolong the shelf life of
CC the therapeutic protein compared to the shelf-life of the therapeutic
CC protein in an unfused state. Human serum albumin (HSA, HA) is responsible
CC for a significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion
CC protein of the invention demonstrates anti-HIV, gastrointestinal-gen.,
CC antidiabetic, anorectic, cardiant and immunosuppressive activities. The
CC fusion protein may be useful for diagnosing, treating, preventing or
CC ameliorating diseases, such as immune disorders, blood disorders,
CC hyperproliferative disorders, renal disorders, cardiovascular disorders,
CC respiratory disorders, angiogenesis-related disorders, neurological
CC disorders, wound healing disorders, endocrine disorders, reproductive
CC disorders, infectious disorders and gastrointestinal disorders, possibly
CC with the use of gene therapy techniques. The current sequence is that of
CC the human fusion-related BNP (brain natriuretic peptide) peptide - SEQ
CC 322 of the invention.
XX XX Sequence 27 AA;
Query Match 100.0%; Score 92; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CFGRKMDRISSSSGLGC 17

Db 10 CFGRKMDRISSSSGLGC 26

RESULT 22

ID ADW45367

XX ADW45367 standard; peptide; 27 AA.

AC ADW45367;

DT 07-APR-2005 (first entry)

DE Human BNP (brain natriuretic peptide) peptide - SEQ ID 371.

XX fusion protein; anti-HIV; gastrointestinal-gen.; antidiabetic; anorectic;

KW nephrotropic; cardiant; cytostatic; neuroprotective; immunosuppressive;

KW immune disorder; hematological disease; hyperproliferative disorder;

KW renal disease; cardiovascular disease; cardiovascular-gen.;

KW respiratory disorder; angiogenesis disorder; neurological disease;

KW wound healing; vulnary; endocrine disease; reproductive disorder;

KW gynecological; infectious disease; antimicrobial;

KW gastrointestinal disease; gene therapy; BNP; brain natriuretic peptide.

XX Homo sapiens.

OS WO2005003296-A2.

PN 13-JAN-2005.

PD 20-JAN-2004; 2004WO-US001369.

XX 22-JAN-2003; 2003US-0441305P.

PR 11-MAR-2003; 2003US-0453201P.

PR 02-MAY-2003; 2003US-0467222P.

PR 23-MAY-2003; 2003US-0472816P.

PR 06-JUN-2003; 2003US-0476267P.

PR 24-SEP-2003; 2003US-0505172P.

PR 30-SEP-2003; 2003US-0506746P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Haseltine WA, Rosen CA;

XX WPI; 2005-091786/10.

DR N-PSDB; ADW45193.

XX New albumin fusion protein for diagnosing, treating or preventing

PT diseases such as HIV/AIDS, diabetes, obesity, heart disease or immune

PT disorders comprises a therapeutic protein (e.g. CD4M33, GLP-2 or PACAP-

PT 27) and an albumin.

XX Example 4; SEQ ID NO 371; 884pp; English.

PS The invention relates to a novel albumin fusion protein comprising a

XX therapeutic protein as listed in the specification in Table 1 and an

CC albumin comprising a sequence of SEQ ID NO: 1, or a fragment or variant

CC of SEQ ID NO: 1, where the fragment or variant has albumin activity and

CC where the albumin activity is the ability to prolong the shelf life of

CC the therapeutic protein compared to the shelf-life of the therapeutic

CC protein in an unfused state. Human serum albumin (HSA, HA) is responsible

CC for a significant proportion of the osmotic pressure of serum and also

CC functions as a carrier of endogenous and exogenous ligands. The fusion

CC protein may be useful for diagnosing, treating, preventing or

CC ameliorating diseases, such as immune disorders, blood disorders,

CC hyperproliferative disorders, renal disorders, cardiovascular disorders,

CC respiratory disorders, angiogenesis-related disorders, neurological

CC disorders, wound healing disorders, endocrine disorders, reproductive

CC disorders, infectious disorders and gastrointestinal disorders, possibly

CC with the use of gene therapy techniques. The current sequence is that of

CC the human BNP (brain natriuretic peptide) peptide - SEQ ID 371 of the

CC invention.

XX Sequence 27 AA;

Query Match 100.0%; Score 92; DB 9; Length 27;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17

Db 10 CFGRKMDRISSSSGLGC 26

RESULT 23

ID ADW45365 standard; peptide; 28 AA.

XX ADW45365;

DT 07-APR-2005 (first entry)

DE Human BNP (brain natriuretic peptide) peptide - SEQ ID 369.

XX fusion protein; anti-HIV; gastrointestinal-gen.; antidiabetic; anorectic;

KW nephrotropic; cardiant; cytostatic; neuroprotective; immunosuppressive;

KW immune disorder; hematological disease; hyperproliferative disorder;

KW renal disease; cardiovascular disease; cardiovascular-gen.;

KW respiratory disorder; angiogenesis disorder; neurological disease;

KW wound healing; vulnary; endocrine disease; reproductive disorder;

KW gynecological; infectious disease; antimicrobial;

KW gastrointestinal disease; gene therapy; BNP; brain natriuretic peptide.

XX Homo sapiens.

OS WO2005003296-A2.

PN 13-JAN-2005.

PD 20-JAN-2004; 2004WO-US001369.

XX 22-JAN-2003; 2003US-0441305P.

PR 11-MAR-2003; 2003US-0453201P.

PR 02-MAY-2003; 2003US-0467222P.

PR 23-MAY-2003; 2003US-0472816P.

PR 06-JUN-2003; 2003US-0476267P.

PR 24-SEP-2003; 2003US-0505172P.

PR 30-SEP-2003; 2003US-0506746P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Haseltine WA, Rosen CA;

XX WPI; 2005-091786/10.

DR N-PSDB; ADW45191.

XX New albumin fusion protein for diagnosing, treating or preventing

PT diseases such as HIV/AIDS, diabetes, obesity, heart disease or immune

PT disorders comprises a therapeutic protein (e.g. CD4M33, GLP-2 or PACAP-

PT 27) and an albumin.

XX Example 4; SEQ ID NO 369; 884pp; English.

PS The invention relates to a novel albumin fusion protein comprising a

XX therapeutic protein as listed in the specification in Table 1 and an

CC albumin comprising a sequence of SEQ ID NO: 1, or a fragment or variant

CC of SEQ ID NO: 1, where the fragment or variant has albumin activity and

CC where the albumin activity is the ability to prolong the shelf life of

CC the therapeutic protein compared to the shelf-life of the therapeutic

CC protein in an unfused state. Human serum albumin (HSA, HA) is responsible

CC for a significant proportion of the osmotic pressure of serum and also

CC functions as a carrier of endogenous and exogenous ligands. The fusion

CC protein may be useful for diagnosing, treating, preventing or

CC ameliorating diseases, such as immune disorders, blood disorders,

CC hyperproliferative disorders, renal disorders, cardiovascular disorders,

CC respiratory disorders, angiogenesis-related disorders, neurological

CC disorders, wound healing disorders, endocrine disorders, reproductive

CC disorders, infectious disorders and gastrointestinal disorders, possibly

CC with the use of gene therapy techniques. The current sequence is that of

CC antidiabetic, anorectic, cardiant and immunosuppressive activities. The
 CC fusion protein may be useful for diagnosing, treating, preventing or
 CC ameliorating diseases, such as immune disorders, blood disorders,
 CC hyperproliferative disorders, renal disorders, cardiovascular disorders,
 CC respiratory disorders, angiogenesis-related disorders, neurological
 CC disorders, wound healing disorders, endocrine disorders, reproductive
 CC disorders, infectious disorders and gastrointestinal disorders, possibly
 CC with the use of gene therapy techniques. The current sequence is that of
 CC the human BNP (brain natriuretic peptide) peptide - SEQ ID 369 of the
 CC invention.
 XX
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 92; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 |||||
 DB 10 CFGRKMDRISSSSGLGC 26
 |||||
 RESULT 24
 ADW45319
 ID ADW45319 standard; peptide; 28 AA.
 XX
 AC ADW45319;
 XX
 DT 07-APR-2005 (first entry)
 DE Human fusion-related BNP (brain natriuretic peptide) peptide - SEQ 323.
 XX
 KW fusion protein; anti-HIV; gastrointestinal-gen.; antidiabetic; anorectic;
 KW nephrotropic; cardiant; cytostatic; neuroprotective; immunosuppressive;
 KW immune disorder; hematological disease; hyperproliferative disorder;
 KW renal disease; cardiovascular disease; hyperproliferative disorder;
 KW respiratory disorder; angiogenesis disorder; cardiovascular disease;
 KW wound healing; vulnary; endocrine disease; reproductive disorder;
 KW gynecological; infectious disease; antimicrobial;
 KW gastrointestinal disease; gene therapy; BNP; brain natriuretic peptide.
 XX
 OS Homo sapiens.
 XX
 PN WO2005003296-A2.
 XX
 PD 13-JAN-2005.
 XX
 PF 20-JAN-2004; 2004WO-US001369.
 XX
 PR 22-JAN-2003; 2003US-0441305P.
 PR 11-MAR-2003; 2003US-0453201P.
 PR 02-MAY-2003; 2003US-0467222P.
 PR 23-MAY-2003; 2003US-0472816P.
 PR 06-JUN-2003; 2003US-0476267P.
 PR 24-SEP-2003; 2003US-0505172P.
 PR 30-SEP-2003; 2003US-0506746P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Haseltine WA, Rosen CA;
 XX
 XX WPI; 2005-091786/10.
 DR N-PSDB; ADW45145.
 XX
 XX New albumin fusion protein for diagnosing, treating or preventing
 PT diseases such as HIV/AIDS, diabetes, obesity, heart disease or immune
 PT disorders comprises a therapeutic protein (e.g. CD4W33, GLP-2 or PACAP-
 PT 27) and an albumin.
 XX
 XX Example 4; SEQ ID NO 323; 884pp; English.
 PS
 CC The invention relates to a novel albumin fusion protein comprising a
 CC therapeutic protein as listed in the specification in Table 1 and an

CC albumin comprising a sequence of SEQ ID NO: 1, or a fragment or variant
 CC of SEQ ID NO: 1, where the fragment or variant has albumin activity and
 CC where the albumin activity is the ability to prolong the shelf life of
 CC the therapeutic protein compared to the shelf-life of the therapeutic
 CC protein in an unfused state. Human serum albumin (HSA, HA) is responsible
 CC for a significant proportion of the osmotic pressure of serum and also
 CC functions as a carrier of endogenous and exogenous ligands. The fusion
 CC protein of the invention demonstrates anti-HIV, gastrointestinal-gen.,
 CC antidiabetic, anorectic, cardiant and immunosuppressive activities. The
 CC fusion protein may be useful for diagnosing, treating, preventing or
 CC ameliorating diseases, such as immune disorders, blood disorders,
 CC hyperproliferative disorders, renal disorders, cardiovascular disorders,
 CC respiratory disorders, angiogenesis-related disorders, neurological
 CC disorders, wound healing disorders, endocrine disorders, reproductive
 CC disorders, infectious disorders and gastrointestinal disorders, possibly
 CC with the use of gene therapy techniques. The current sequence is that of
 CC the human fusion-related BNP (brain natriuretic peptide) peptide - SEQ
 CC 323 of the invention.
 XX
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 92; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 |||||
 DB 10 CFGRKMDRISSSSGLGC 26
 |||||
 RESULT 25
 ADP49272
 ID ADP49272 standard; peptide; 29 AA.
 XX
 AC ADP49272;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Natriuretic compound polypeptide #15.
 XX
 KW cardiant; hypotensive; natriuretic compound; heart failure; hypertension;
 KW extracellular fluid.
 XX
 OS Synthetic.
 XX
 PN WO2004047871-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 12-NOV-2003; 2003WO-US037996.
 XX
 PR 26-NOV-2002; 2002US-0429151P.
 XX
 PA (NOBE-) NOBEX CORP.
 XX
 PI James KD, Radhakrishnan B, Malkar NB, Miller MA, Ekwuribe NN;
 XX
 DR WPI; 2004-450218/42.
 XX
 PT Natriuretic compound conjugate useful in the treatment of e.g. congestive
 PT heart failure, comprises natriuretic compound and at least one modifying
 PT moiety.
 XX
 XX Claim 18; Page 93; 125pp; English.
 PS
 CC The present invention relates to a natriuretic compound, which comprises
 CC a natriuretic compound containing a natriuretic molecule NPR-A
 CC (natriuretic peptide receptor-A) binding site and at least one modifying
 CC moiety conjugation site, and at least one modifying moiety attached to
 CC the modifying moiety conjugation site. The conjugates are used for the
 CC treatment of a condition involving an excess level of extracellular fluid
 CC e.g. chronic or acute congestive heart failure and hypertension. The
 CC present sequence is a peptide shown in the invention.

```

XX SQ Sequence 29 AA;
Query Match 100.0%; Score 92; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSGLGC 17
Db 10 CFGRKMDRISSSGLGC 26

RESULT 26
ADP49302
ID ADP49302 standard; peptide; 29 AA.
XX AC
XX ADP49302;
XX DT 26-AUG-2004 (first entry)
XX DE
XX Natriuretic compound polypeptide #45.
XX KW cardiant; hypotensive; natriuretic compound; heart failure; hypertension;
XX KW extracellular fluid.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 3 /note= "Xaa-any amino acid except Lys"
XX FT
XX PN WO2004047871-A2.
XX PD 10-JUN-2004.
XX PF 12-NOV-2003; 2003WO-US037996.
XX PR 26-NOV-2002; 2002US-0429151P.
XX PA (NOBE-) NOBEX CORP.
XX PI James KD, Radhakrishnan B, Malkar NB, Miller MA, Ekwuribe NN;
XX WPI; 2004-450218/42.
XX Natriuretic compound conjugate useful in the treatment of e.g. congestive
XX heart failure, comprises natriuretic compound and at least one modifying
XX moiety.
XX Example 25; Page 77; 125pp; English.
XX The present invention relates to a natriuretic compound, which comprises
XX a natriuretic compound containing a natriuretic molecule NPR-A
XX (natriuretic peptide receptor-A) binding site and at least one modifying
XX moiety conjugation site, and at least one modifying moiety attached to
XX the modifying moiety conjugation site. The conjugates are used for the
XX treatment of a condition involving an excess level of extracellular fluid
XX e.g. chronic or acute congestive heart failure and hypertension. The
XX present sequence is a peptide shown in the invention.
XX SQ Sequence 29 AA;
Query Match 100.0%; Score 92; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSGLGC 17
Db 10 CFGRKMDRISSSGLGC 26

RESULT 27
ADW45311
ID ADW45311 standard; peptide; 29 AA.
XX AC
XX ADW45311;
XX DT 07-APR-2005 (first entry)
XX DE
XX Human fusion-related BNP (brain natriuretic peptide) peptide - SEQ 315.
XX KW fusion protein; anti-HIV; gastrointestinal-gen.; antidiabetic; anorectic;
XX KW nephrotropic; cardiant; cytostatic; neuroprotective; immunosuppressive;
XX KW immune disorder; hematological disease; hyperproliferative disorder;
XX KW renal disease; cardiovascular disease; cardiovascular-gen.;
XX KW respiratory disorder; angiogenesis disorder; neurological disease;
XX KW wound healing; vulnery; endocrine disease; reproductive disorder;
XX KW gynecological; infectious disease; antimicrobial;
XX KW gastrointestinal disease; gene therapy; BNP; brain natriuretic peptide.
XX OS Homo sapiens.
XX PN WO2005003296-A2.
XX PD 13-JAN-2005.
XX PF 20-JAN-2004; 2004WO-US001369.
XX PR 22-JAN-2003; 2003US-0441305P.
XX PR 11-MAR-2003; 2003US-0453201P.
XX PR 02-MAY-2003; 2003US-0467222P.
XX PR 23-MAY-2003; 2003US-0472816P.
XX PR 06-JUN-2003; 2003US-0476267P.
XX PR 24-SEP-2003; 2003US-0505172P.
XX PR 30-SEP-2003; 2003US-0506746P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Haseltine WA, Rosen CA;
XX WPI; 2005-091786/10.
XX N-PSDB; ADW45137.
XX New albumin fusion protein for diagnosing, treating or preventing
XX diseases such as HIV/AIDS, diabetes, obesity, heart disease or immune
XX disorders comprises a therapeutic protein (e.g. CD4M33, GLP-2 or PACAP-
XX 27) and an albumin.
XX Example 4; SEQ ID NO 315; 884pp; English.
XX The invention relates to a novel albumin fusion protein comprising a
XX therapeutic protein as listed in the specification in Table 1 and an
XX albumin comprising a sequence of SEQ ID NO: 1, or a fragment or variant
XX of SEQ ID NO: 1, where the fragment or variant has albumin activity and
XX where the albumin activity is the ability to prolong the shelf life of
XX the therapeutic protein compared to the shelf-life of the therapeutic
XX protein in an unfused state. Human serum albumin (HSA, HA) is responsible
XX for a significant proportion of the osmotic pressure of serum and also
XX functions as a carrier of endogenous and exogenous ligands. The fusion
XX protein of the invention demonstrates anti-HIV, gastrointestinal-gen.,
XX antidiabetic, anorectic, cardiant and immunosuppressive activities. The
XX fusion protein may be useful for diagnosing, treating, preventing or
XX ameliorating diseases, such as immune disorders, blood disorders,
XX hyperproliferative disorders, renal disorders, cardiovascular disorders,
XX respiratory disorders, angiogenesis-related disorders, neurological
XX disorders, wound healing disorders, endocrine disorders, reproductive
XX disorders, infectious disorders and gastrointestinal disorders, possibly
XX with the use of gene therapy techniques. The current sequence is that of
XX the human fusion-related BNP (brain natriuretic peptide) peptide - SEQ
XX 315 of the invention.
XX SQ Sequence 29 AA;
Query Match 100.0%; Score 92; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CFGRKMDRISSSSGLGC 17
 DB 10 CFGRKMDRISSSSGLGC 26

RESULT 28
 ADW45310
 ID ADW45310 standard; peptide; 29 AA.

XX AC ADW45310;
 XX DT 07-APR-2005 (first entry)
 XX DE

Human fusion-related BNP (brain natriuretic peptide) peptide - SEQ 314.
 XX fusion protein; anti-HIV; gastrointestinal-gen.; antidiabetic; anorectic;
 KW nephrotropic; cardiac; cytostatic; neuroprotective; immunosuppressive;
 KW immune disorder; hematological disease; hyperproliferative disorder;
 KW renal disease; cardiovascular disease; cardiovascular-gen.;
 KW respiratory disorder; angiogenesis disorder; neurological disease;
 KW wound healing; vulnary; endocrine disease; reproductive disorder;
 KW gynecological; infectious disease; antimicrobial;
 KW gastrointestinal disease; gene therapy; BNP; brain natriuretic peptide.

XX Homo sapiens.

XX WO2005003296-A2.

XX 13-JAN-2005.

XX 20-JAN-2004; 2004WO-US001369.

XX 22-JAN-2003; 2003US-0441305P.

PR 11-MAR-2003; 2003US-0453201P.

PR 02-MAY-2003; 2003US-0467222P.

PR 23-MAY-2003; 2003US-0472816P.

PR 06-JUN-2003; 2003US-0476267P.

PR 24-SEP-2003; 2003US-0505172P.

PR 30-SEP-2003; 2003US-0506746P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Haseltine WA, Rosen CA;

XX WPI; 2005-091786/10.

XX N-PSDB; ADW45136.

XX New albumin fusion protein for diagnosing, treating or preventing

PT diseases such as HIV/AIDS, diabetes, obesity, heart disease or immune
 PT disorders comprises a therapeutic protein (e.g. CD4M33, GLP-2 or PACAP-
 PT 27) and an albumin.
 XX
 PS Example 4; SEQ ID NO 314; 884pp; English.
 XX
 CC The invention relates to a novel albumin fusion protein comprising a
 CC therapeutic protein as listed in the specification in Table 1 and an
 CC albumin comprising a sequence of SEQ ID NO: 1, or a fragment or variant
 CC of SEQ ID NO: 1, where the fragment or variant has albumin activity and
 CC where the albumin activity is the ability to prolong the shelf life of
 CC the therapeutic protein compared to the shelf-life of the therapeutic
 CC protein in an unfused state. Human serum albumin (HSA, HA) is responsible
 CC for a significant proportion of the osmotic pressure of serum and also
 CC functions as a carrier of endogenous and exogenous ligands. The fusion
 CC protein of the invention demonstrates anti-HIV, gastrointestinal-gen.,
 CC antidiabetic, anorectic, cardiac and immunosuppressive activities. The
 CC fusion protein may be useful for diagnosing, treating, preventing or
 CC ameliorating diseases, such as immune disorders, blood disorders,
 CC hyperproliferative disorders, renal disorders, cardiovascular disorders,
 CC respiratory disorders, angiogenesis-related disorders, neurological
 CC disorders, wound healing disorders, endocrine disorders, reproductive
 CC disorders, infectious disorders and gastrointestinal disorders, possibly
 CC with the use of gene therapy techniques. The current sequence is that of

CC the human fusion-related BNP (brain natriuretic peptide) peptide - SEQ
 CC 314 of the invention.
 XX
 SQ Sequence 29 AA;

Query Match 100.0%; Score 92; DB 9; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 DB 10 CFGRKMDRISSSSGLGC 26

RESULT 29

AAR34302
 ID AAR34302 standard; protein; 31 AA.

XX AC AAR34302;

XX DT 28-JUL-1993 (first entry)

XX DE Mutated BNP.

XX KW Wild type; brain natriuretic peptide; BNP; modify; Asp-Pro.

XX OS Homo sapiens.

XX PN JP05056794-A.

XX PD 09-MAR-1993.

XX PF 03-SEP-1991; 91JP-00222783.

XX PR 03-SEP-1991; 91JP-00222783.

XX PA (DAI-) DAIICHI KAGAKU YAKUIN KK.

XX PA (DAUC) DAIICHI PHARM CO LTD.

XX DR WPI; 1993-120386/15.

XX PT Physiologically active peptide prepn. e.g. human brain natriuretic
 PT peptide - By culturing transformed cells having gene which encodes fused
 PT protein of active and protective peptide(s), collecting and cleaving
 PT protein.

XX PS Disclosure; Page 7; 16pp; Japanese.

XX CC The sequences given in AAR34301-02 are mutated brain natriuretic peptides
 CC (BNP). These peptides have been modified such that the Asp in the N-
 CC terminal Asp-Pro linkage may be replaced by Ser or may be deleted

XX SQ Sequence 31 AA;

Query Match 100.0%; Score 92; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 DB 9 CFGRKMDRISSSSGLGC 25

RESULT 30

AAR40861
 ID AAR40861 standard; protein; 32 AA.

XX AC AAR40861;

XX DT 14-MAR-1994 (first entry)

XX DE BNP.

XX

KW BNP; brain natriuretic peptide; transformation; expression; cloning;
 KW puc119; protease V8.
 XX
 OS Homo sapiens.
 PN JP05207891-A.
 XX
 PD 20-AUG-1993.
 XX
 PF 08-MAR-1991; 91JP-00043641.
 XX
 PR 08-MAR-1991; 91JP-00043641.
 XX
 PA (SHIO) SHIONOGI & CO LTD.
 XX
 DR WPI; 1993-297469/38.
 DR N-PSDB; AAQ47829.
 XX
 PT Brain natriuretic peptide prepn. - by forming fused peptide contg.
 PT desired sequence, cleaving with restriction enzyme and collecting desired
 PT peptide.
 XX
 PS Disclosure; Page 8; 11pp; Japanese.
 XX
 CC The prepn. of BNP comprises: (a) obtaining a fused protein protein of
 CC formula X-Glu-BNP, where X is a leader sequence of 70-170 amino acids
 CC (AA45761); (b) cleaving the fused protein with a restriction enzyme that
 CC can cleave between Glu and BNP. (c) collecting BNP. The BNP sequence is
 CC shown in (AAQ47829) and the Glu-BNP sequence is given in (AAQ47831)
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 92; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 DB 10 CFGRKMDRISSSSGLGC 26
 RESULT 31
 AAR34301
 ID AAR34301 standard; protein; 32 AA.
 AC AAR34301;
 XX
 DT 28-JUL-1993 (first entry)
 XX
 DE Mutated hBNP.
 XX
 KW Wild type; brain natriuretic peptide; BNP; modify; Asp-Pro.
 XX
 OS Homo sapiens.
 XX
 PN JP05056794-A.
 XX
 PD 09-MAR-1993.
 XX
 PF 03-SEP-1991; 91JP-00222783.
 XX
 PR 03-SEP-1991; 91JP-00222783.
 XX
 PA (DAII-) DAIICHI KAGAKU YAKUHHN KK.
 PA (DAUC) DAIICHI PHARM CO LTD.
 XX
 DR WPI; 1993-120386/15.
 XX
 PT Physiologically active peptide prepn. e.g. human brain natriuretic
 PT peptide - by culturing transformed cells having gene which encodes fused
 PT protein of active and protective peptide(s), collecting and cleaving
 PT protein.
 XX

PS Disclosure; Page 6; 16pp; Japanese.
 XX
 CC The sequences given in AAR34301-02 are mutated brain natriuretic peptides
 CC (BNP). These peptides have been modified such that the Asp in the N-
 CC terminal Asp-Pro linkage may be replaced by Ser or may be deleted
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 92; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 DB 10 CFGRKMDRISSSSGLGC 26
 RESULT 32
 AAR36381
 ID AAR36381 standard; protein; 32 AA.
 AC AAR36381;
 XX
 DT 29-JUL-1993 (first entry)
 XX
 DE Recombinant hBNP.
 XX
 KW Plasmid; fusion peptide; murine; rat; interleukin 1; IL-1; human;
 KW brain natriuretic peptide; hBNP; recombinant; BNP.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "May be absent"
 FT
 XX
 PN JP05068581-A.
 XX
 PD 23-MAR-1993.
 XX
 PF 10-SEP-1991; 91JP-00230597.
 XX
 PR 10-SEP-1991; 91JP-00230597.
 XX
 PA (DAII-) DAIICHI KAGAKU YAKUHHN KK.
 PA (DAUC) DAIICHI PHARM CO LTD.
 XX
 DR WPI; 1993-130645/16.
 XX
 PT Prepn. of physiologically active peptide without aspartic acid-proline
 PT sequence - comprises gene recombination with cell transformation by
 PT specified expression vector.
 XX
 PS Claim 3; Page 6; 17pp; Japanese.
 XX
 CC This sequence represent a recombinant human brain natriuretic peptide
 CC (hBNP). This protein was encoded by the fragments of plasmids given in
 CC Q4110-04 which encode fusion peptides of murine or rat interleukin 1 (IL-
 CC 1) fused to hBNP. Fusion genes of this kind can be used to express
 CC recombinant BNP which lacks the Asp-Pro N-terminal bond. The Asp residue
 CC may be replaced by Ser or may be absent
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 92; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 DB 10 CFGRKMDRISSSSGLGC 26

```

RESULT 33
AAW70090
ID AAW70090 standard; peptide; 32 AA.
XX
AC AAW70090;
XX
DT 28-OCT-1998 (first entry)
XX
DE Brain natriuretic peptide (BNP) 1.
XX
KW BNP; brain natriuretic peptide; cardiac disease; cardiac hypertrophy;
KW chronic heart failure; ischaemic cardiac disease; arrhythmia; cGMP;
KW pulmonary blood circulation; haemodynamic property.
XX
OS Unidentified.
XX
XX WO9834636-A1.
XX
XX 13-AUG-1998.
XX
XX 05-FEB-1998; 98WO-JP000483.
XX
XX 05-FEB-1997; 97JP-00022594.
XX
XX (SUNR ) SUNTORY LTD.
XX
XX Inomata N, Yamaki A, Furuya M, Hidaka T;
XX
XX WPI; 1998-446949/38.
XX
XX Drug composition comprises natriuretic peptide(s) - for safe treatment of
XX cardiac hypertrophy associated diseases and chronic heart failure.
XX
XX Example; Page 23; 35pp; Japanese.
XX
XX This represents a brain natriuretic peptide (BNP) sequence. The invention
XX provides a composition for treating cardiac diseases associated with
XX cardiac hypertrophy. The composition comprises an active ingredient
XX capable of binding to the peptide receptor of GC-A and promoting
XX production of cGMP. The drug composition may be used clinically to treat
XX cardiac diseases caused by cardiac hypertrophy, including chronic heart
XX failure, ischaemic cardiac diseases and arrhythmia. The active substance
XX can bind to the natriuretic peptide receptor of GC-A and promote
XX production of cGMP, effectively preventing cardiac hypertrophy and
XX leading to improvement of the pulmonary blood circulation. The substance
XX does not affect haemodynamic properties, blood pressure, heart beat and
XX urine volume
XX
XX Sequence 32 AA;

Query Match 100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
    |||||
Db 10 CFGRKMDRISSSSGLGC 26
    |||||

RESULT 34
AAW67040
ID AAW67040 standard; peptide; 32 AA.
XX
AC AAW67040;
XX
DT 15-DEC-1998 (first entry)
XX
DE Brain natriuretic peptide (BNP).
XX
KW atrial natriuretic peptide; brain natriuretic peptide; ANP; BNP;
KW lipophilic substituent; hypertension; congestive heart failure; oedema;
KW renal disorder.
XX

```

```

OS Mammalia.
XX
XX Key
XX Region
XX
XX Region
XX
XX Region
XX
XX Region
XX
XX Region
XX
XX Region
XX
XX Region
XX
XX Disulfide-bond 10. .26
XX
XX WO9845329-A1.
XX
XX 15-OCT-1998.
XX
XX 06-APR-1998; 98WO-DK000142.
XX
XX 04-APR-1997; 97US-0043400P.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Huusfeldt PO, Madsen K, Knudsen LB;
XX
XX WPI; 1998-557474/47.
XX
XX Lipophilic derivatives of atrial and brain natriuretic peptides - notably
XX as amides, prolong activity, use in hypertension, congestive heart
XX failure, renal disorders, oedema, and hepatic cirrhosis.
XX
XX Claim 32; Page 1-2; 23pp; English.
XX
XX The invention relates to natriuretic derivatives, containing a lipophilic
XX substituent attached to any one amino acid residue. Also new are
XX natriuretic derivatives as above, but with two attached lipophilic
XX substituents. Atrial natriuretic (ANP) and brain natriuretic (BNP)
XX peptides are already used in treatment of various diseases, and it is
XX believed that the lipophilic derivatives will have similar uses. These
XX diseases include hypertension, congestive heart failure, oedema, renal
XX disorders, and hepatic cirrhosis. The lipophilic group protects the
XX peptide from metabolic breakdown, increasing the duration of action. The
XX present sequence represents BNP
XX
XX Sequence 32 AA;

Query Match 100.0%; Score 92; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
    |||||
Db 10 CFGRKMDRISSSSGLGC 26
    |||||

RESULT 35

```

AA82550
ID AAB82550 standard; peptide; 32 AA.
XX
AC AAB82550;
DT 17-SEP-2001 (first entry)
XX
DE Human brain natriuretic peptide.
XX
DE Brain natriuretic peptide; BNP; Dendroaspis natriuretic peptide; DNP;
KW human; snake venom; diuretic; vasodilator; renin-suppressor;
KW heart failure; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 10..25
XX
PN WO200144284-A2.
XX
PD 21-JUN-2001.
XX
XX 15-DEC-2000; 2000WO-US034080.
PF
XX 17-DEC-1999; 99US-00466268.
PR
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PA
XX Burnett J, Lisy O;
PI
XX WPI; 2001-457339/49.
DR
XX
XX Fusion peptides comprising Dendroaspis natriuretic peptides, useful for
PT treating heart failure and as vasodilators, renin-suppressors and
PT natriuretics or diuretics.
PT
PS Disclosure; Fig 1; 81pp; English.
XX
XX The present sequence is that of human brain natriuretic peptide (BNP).
CC The invention provides fusion peptides comprising a biologically active
CC portion of Dendroaspis natriuretic peptide (DNP). DNP is obtained from
CC the venom of the green mamba snake, Dendroaspis angusticeps. It contains
CC a 17-amino acid disulfide ring structure similar to that of BNP. Claimed
CC methods of treating, inhibiting or preventing heart failure in a mammal
CC (human, rat, mouse, dog, cattle, horse, sheep, goat or cat) involve
CC administering DNP or a chimeric peptide including a portion of DNP (see
CC AAB82543 and AAB82544) and the N-terminal portion of especially human BNP
CC or C-type natriuretic peptide. Such peptides may also be used to treat
CC acute or chronic kidney failure, hypertension, cirrhosis of the liver,
CC nephrotic syndrome and other oedematous states
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 10 CFGRKMDRISSSSGLGC 26
RESULT 36
AAB91333
ID AAB91333 standard; peptide; 32 AA.
XX
AC AAB91333;
XX
DT 22-JUN-2001 (first entry)
XX
DE Brain natriuretic peptide (BNP) SEQ ID NO:509.
DE Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW

KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI
XX WPI; 2001-112059/12.
DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
PT
XX Disclosure; Page 366; 733pp; English.
PS
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 10 CFGRKMDRISSSSGLGC 26
RESULT 37
AAB91340
ID AAB91340 standard; peptide; 32 AA.
XX
AC AAB91340;
XX
XX 22-JUN-2001 (first entry)
DT
XX Brain natriuretic peptide (BNP) SEQ ID NO:516.
DE
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX

PN WO200069900-A2.
 XX 23-NOV-2000.
 XX 17-MAY-2000; 2000WO-US013576.
 XX 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX (CONJ-) CONJUCHEM INC.
 PA Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX WPI; 2001-112059/12.
 XX
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 369; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxy/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 92; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 |||||
 Db 10 CFGRKMDRISSSSGLGC 26
 |||||
 RESULT 38
 AAB45739
 ID AAB45739 standard; protein; 32 AA.
 XX
 AC AAB45739;
 XX
 DT 15-MAR-2001 (first entry)
 XX
 DE Human mature BNP.
 XX
 KW BNP; brain natriuretic peptide; heart failure; vascular stenosis; DNP;
 KW D-type natriuretic peptide; antiarteriosclerotic; cardiant; vasospasm;
 KW antihypertensive; cardiac muscle; pulmonary hypertension; human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 10. .26
 XX
 PN WO200071576-A2.
 XX
 PD 30-NOV-2000.
 XX
 PF 24-MAY-2000; 2000WO-US014351.
 XX
 PR 24-MAY-1999; 99US-0135490P.
 XX

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 (SIMA/) SIMARI R.
 XX Simari R;
 XX WPI; 2001-025135/03.
 DR N-PSDB; AAC82677.
 XX
 PT Inhibiting or preventing heart failure, hypertension and atherosclerosis,
 PT involves administering a composition comprising a nucleic acid molecule
 PT encoding brain natriuretic peptide in a delivery vehicle.
 XX
 PS Disclosure; Page 80; 83pp; English.
 XX
 CC This invention describes a novel method for inhibiting or preventing (I)
 CC heart failure in a mammal, by administering a composition containing a
 CC nucleic acid molecule (NAM) comprising a nucleic acid segment encoding
 CC brain natriuretic peptide (BNP), D-type natriuretic peptide (DNP) or its
 CC chimera, in a delivery vehicle. The invention also describes (1) an
 CC isolated and purified NAM (II) comprising a nucleic acid segment encoding
 CC a chimeric natriuretic peptide containing at least a portion of DNP; (2)
 CC an adeno-associated virus vector (III) comprising a NAM containing a
 CC nucleic acid segment encoding BNP, DNP or its chimera operably linked to
 CC transcriptional regulatory elements; (3) an adenovirus vector (IV)
 CC comprising a NAM containing a nucleic acid segment encoding DNP or its
 CC chimera operably linked to transcriptional regulatory elements; and (4) a
 CC composition comprising (II), (III), or (IV) and a delivery vehicle. The
 CC products of the invention have antiarteriosclerotic, cardiant and
 CC antihypertensive activity. The method is useful for inhibiting or
 CC preventing heart failure in a mammal and also to relax cardiac muscle, to
 CC increase BNP levels in a mammal, to detect progression of heart failure
 CC in a mammal subjected to brain natriuretic gene therapy, to inhibit or
 CC prevent vasospasm and pulmonary hypertension in a mammal. DNP and BNP are
 CC also useful for inhibiting or preventing atherosclerosis and vascular
 CC restenosis
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 92; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 |||||
 Db 10 CFGRKMDRISSSSGLGC 26
 |||||
 RESULT 39
 AAE12434
 ID AAE12434 standard; peptide; 32 AA.
 XX
 AC AAE12434;
 XX
 DT 03-JAN-2002 (first entry)
 XX
 DE Human brain natriuretic peptide (BNP).
 XX
 KW Prophylaxis; ischaemic heart disease; myocardial infarction; human;
 KW ischaemia reperfusion injury; ischaemic heart disease; infarct region;
 KW vasotropic; brain natriuretic peptide; BNP.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 10. .26
 XX
 PN US2001027181-A1.
 XX
 PD 04-OCT-2001.
 XX
 PF 03-JAN-2001; 2001US-00752724.
 XX

PR 31-MAR-2000; 2000JP-00098134.
 XX (KITA/) KITAKAZE M.
 XX
 XX
 XX Kitakaze M;
 XX
 XX WPI; 2001-638528/73.
 XX
 XX Composition for the treatment or prophylaxis of ischemic heart disease
 PT i.e. myocardial infarction, comprises a substance which can increase
 PT intracellular cGMP production by acting on a natriuretic peptide
 PT receptor.
 XX
 XX Disclosure; Page 4; 9pp; English.
 XX
 XX The invention relates to a pharmaceutical composition for the treatment
 CC or prophylaxis of ischaemic heart disease, comprises a substance as an
 CC active ingredient, which can increase intracellular cGMP production by
 CC acting on a natriuretic peptide receptor and which has an effect of
 CC reducing an infarct region. The composition is useful for suppressing
 CC ischaemia reperfusion injury in the treatment of ischaemic heart disease,
 CC preferably myocardial infarction. The present sequence is human brain
 CC natriuretic peptide (BNP)
 XX
 XX Sequence 32 AA;
 SQ
 Query Match 100.0%; Score 92; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 Db |||||
 10 CFGRKMDRISSSSGLGC 26
 RESULT 40
 AAB70810
 ID AAB70810 standard; peptide; 32 AA.
 XX
 XX
 XX AAB70810;
 XX
 XX 08-JUN-2001 (first entry)
 DT
 XX Human natriuretic peptide BNP.
 DE
 XX Natriuretic peptide; BNP; antibiotic; veterinary; medicine; skin;
 KW food technology; natriuretic; bacterial flora; gastrointestinal tract;
 KW respiratory system; urogenital system; adjuvant; fermentation; human;
 KW preservatives; dermatological; antiinflammatory; antidiarrheic; brain;
 KW antibiotic; infant diarrhoea; skin disorder.
 XX
 XX Homo sapiens.
 OS
 XX DE19942230-A1.
 PN
 XX 15-MAR-2001.
 PD
 XX 03-SEP-1999; 99DE-01042230.
 PF
 XX 03-SEP-1999; 99DE-01042230.
 PR
 XX (FORS/) FORSSMANN W.
 XX
 XX Krause A, Maronde E, Forssmann W;
 PI
 XX WPI; 2001-258920/27.
 XX
 XX Use of natriuretic peptides as antibiotics in medicine and food
 PT technology.
 PT
 XX Disclosure; Col 2-3; 4pp; German.
 XX
 XX This invention describes a novel use of natriuretic peptides as

CC antibiotics in human and veterinary medicine and in food technology. Pure
 CC natriuretic peptides (natriuretics) are used as antibiotics: (a) or the
 CC treatment of pathogenically altered bacterial flora in the
 CC gastrointestinal tract, respiratory or urogenital system or skin; and (b)
 CC in food technology as adjuvants in fermentation processes and
 CC preservatives. The products of the invention have dermatological,
 CC antiinflammatory, antidiarrheic and antibiotic activity. The peptides
 CC improve the bacterial flora of the body and can be used for the control
 CC of diarrhoea, especially in infants, as well as intestinal, respiratory
 CC tract, urogenital and skin infections. They are preferably used for the
 CC treatment of skin disorders caused by microbes and problems caused by
 CC abnormal human vaginal flora. They are also useful as preservatives in
 CC foodstuffs, especially those which have been produced by fermentation.
 CC This sequence represents the human BNP peptide used in the method of the
 CC invention
 XX
 XX Sequence 32 AA;
 SQ
 Query Match 100.0%; Score 92; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 Db |||||
 10 CFGRKMDRISSSSGLGC 26
 RESULT 41
 ABG98205
 ID ABG98205 standard; peptide; 32 AA.
 XX
 XX AC ABG98205;
 XX
 XX 08-JAN-2003 (first entry)
 DT
 XX Human brain natriuretic peptide (BNP-32).
 DE
 XX Human; natriuretic peptide; NP; endochondral ossification;
 KW bone formation; cartilage; bone; signalling pathway; FGF;
 KW fibroblast growth factor; cardiovascular homeostasis; diuresis;
 KW natriuresis; vasodilation; atrial natriuretic peptide; ANP;
 KW brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP;
 KW dendroaspis natriuretic peptide; DNP; NPR-A; NPR-B;
 KW guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP;
 KW skeletal dysplasia; achondroplasia; osteopathia.
 XX
 XX Homo sapiens.
 OS
 XX WO200274234-A2.
 PN
 XX 26-SEP-2002.
 PD
 XX 20-MAR-2002; 2002WO-IL000229.
 PF
 XX 20-MAR-2001; 2001IL-00142118.
 PR
 XX 20-MAR-2001; 2001US-0276939P.
 XX
 XX (PROC-) PROCHON BIOTECH LTD.
 PA
 XX Golembio M, Yayon A;
 PI
 XX WPI; 2002-750515/81.
 DR
 XX Pharmaceutical composition useful in the treatment of skeletal dysplasias
 PT e.g. achondroplasia comprises at least one natriuretic peptide.
 PT
 XX Claim 4; Fig 3; 41pp; English.
 PS
 XX The invention discloses a pharmaceutical composition comprising at least
 CC one natriuretic peptide (NP), or its variant, and a carrier or excipient.
 CC Endochondral ossification is a fundamental mechanism for bone formation,
 CC whereby cartilage is replaced by bone. Endochondral ossification is the
 CC result of the concerted action of several signalling pathways, most

CC notably the pathway triggered by the activation of the fibroblast growth
 CC factor (FGF). Natriuretic peptides are also known for their role in
 CC cardiovascular homeostasis, diuresis, natriuresis and vasodilation. Four
 CC isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic
 CC peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaspis
 CC natriuretic peptide (DNP). NP's effect their biological role through two
 CC receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains
 CC which are activated upon ligand binding and lead to accumulation of
 CC intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and
 CC inhibition of the NEPs increases the concentration of the NPs in the
 CC circulation. The invention discloses compositions comprising NP secreting
 CC cells and methods for treating skeletal dysplasias involving
 CC transplanting or implanting the natriuretic peptide secreting cells. The
 CC NP secreting cells are useful in the manufacture of a medicament for the
 CC treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of
 CC abnormal bone and for increasing the size of bone growth plate in
 CC abnormal bone (e.g. limb bone). The compositions induce bone elongation
 CC in abnormal bone growth and enhance NP stabilisation in circulation. The
 CC sequences presented in ABG98202-ABG98272 are the CNP peptide and
 CC variants, with differing levels of activity, designed from it. The
 CC degenerate peptide is presented in ABG98206
 XX
 SQ Sequence 32 AA;

Query Match 100.0%; Score 92; DB 5; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGCG 17
 |||||
 Db 10 CFGRKMDRISSSSLGCG 26

RESULT 42
 ADA00765
 ID ADA00765 standard; peptide; 32 AA.
 XX ADA00765;
 XX 06-NOV-2003 (first entry)
 XX Human natriuretic peptide BNP.
 XX Human, natriuretic protein; atrial natriuretic peptide; ANP; ANF;
 KW hypotensive; hepatotropic; nephrotropic; cardiant; vasodilator;
 KW hepatotropic; respiratory; clearance receptor;
 KW natriuretic peptide receptor; hNPR-C; hANP (1-28); human A receptor;
 KW hNPR-A; neutral endopeptidase 11.24; NEP; natriuresis; diuresis;
 KW vasodilation; renin-angiotensin II; aldosterone; electrolyte imbalance;
 KW hypertension; renovascular hypertension; congestive heart failure; CHF;
 KW nephrotic syndrome; hepatic cirrhosis; pulmonary disease; renal failure;
 KW uroilatin.
 XX Homo sapiens.
 XX US6525022-B1.
 XX 25-FEB-2003.
 XX 16-SEP-1998; 98US-00154390.
 XX 12-NOV-1993; 93US-00152994.
 PR 04-NOV-1994; 94WO-US012591.
 PR 06-JAN-1995; 95US-00362552.
 PR 11-APR-1995; 95US-00419877.
 PR 06-JUN-1995; 95US-00470846.
 XX (GETH) GENENTECH INC.
 XX Lowe DG, Cunningham BC, Oare D, McDowell RS, Burnier JP;
 XX WPI; 2003-553629/52.
 XX

PT Novel variant of atrial natriuretic factor, useful as therapeutic agent
 PT for treating hypertension, congestive heart failure, nephrotic syndrome,
 PT hepatic cirrhosis, pulmonary disease and renal failure.
 XX
 PS Disclosure; Fig 1; 51pp; English.
 XX
 CC The invention relates to an atrial natriuretic factor (ANF, also known as
 CC ANP, a natriuretic peptide) comprising one or more amino acid
 CC substitutions selected from Gly9Thr, Gly9a, Gly9Arg, Arg11Ser, Arg11Asp,
 CC Gly16Arg, Gly16Gly, Gly16Gln, Gly16His, and Gly16p-amidinophenyl Ala.
 CC Also included is a composition comprising nucleic acid encoding the ANF
 CC variant. The ANF has a decreased binding affinity for the human clearance
 CC receptor, natriuretic peptide receptor (hNPR)-C, compared to wild-type
 CC hANP (1-28) and an equal or higher binding affinity for the human A
 CC receptor, hNPR-A, compared to wild-type hANP (1-28). The binding affinity
 CC for hNPR-C is less than 50% or 10% of the affinity of wild-type ANF. The
 CC ANF variant has an increased half-life relative to wild-type hANP (1-28)
 CC when incubated with neutral endopeptidase 11.24 (NEP). The ANF variant is
 CC useful for inducing natriuresis, diuresis or vasodilation or inhibit
 CC renin-angiotensin II and aldosterone release and as therapeutic agents in
 CC the treatment of various pathological conditions associated with water or
 CC electrolyte imbalance and hypertension, especially renovascular
 CC hypertension, congestive heart failure (CHF), nephrotic syndrome and
 CC hepatic cirrhosis, pulmonary disease and renal failure due to ineffective
 CC renal perfusion or reduced glomerular filtration rate, to modulate the
 CC activity of other diuretic, natriuretic or vasorelaxant compounds by
 CC binding to alternate receptors, stimulating receptor turnover, or
 CC providing alternate substrates for degradative enzyme of receptor
 CC activity and inhibiting these enzymes or receptors. The present sequence
 CC is a human natriuretic peptide.
 XX
 SQ Sequence 32 AA;

Query Match 100.0%; Score 92; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGCG 17
 |||||
 Db 10 CFGRKMDRISSSSLGCG 26

RESULT 43
 ADA00784
 ID ADA00784 standard; peptide; 32 AA.
 XX ADA00784;
 XX 06-NOV-2003 (first entry)
 XX Human natriuretic peptide BNP 1-28.
 XX Human, natriuretic protein; atrial natriuretic peptide; ANP; ANF;
 KW hypotensive; hepatotropic; nephrotropic; cardiant; vasodilator;
 KW hepatotropic; respiratory; clearance receptor;
 KW natriuretic peptide receptor; hNPR-C; hANP (1-28); human A receptor;
 KW hNPR-A; neutral endopeptidase 11.24; NEP; natriuresis; diuresis;
 KW vasodilation; renin-angiotensin II; aldosterone; electrolyte imbalance;
 KW hypertension; renovascular hypertension; congestive heart failure; CHF;
 KW nephrotic syndrome; hepatic cirrhosis; pulmonary disease; renal failure;
 KW mutant; mutein.
 XX Synthetic.
 OS Homo sapiens.
 XX US6525022-B1.
 XX 25-FEB-2003.
 XX 16-SEP-1998; 98US-00154390.
 XX 12-NOV-1993; 93US-00152994.
 PR 04-NOV-1994; 94WO-US012591.
 PR

PR 06-JAN-1995; 95US-00362552.
 PR 11-APR-1995; 95US-00419877.
 PR 06-JUN-1995; 95US-00470846.
 XX (GETH) GENENTECH INC.
 PA Lowe DG, Cunningham BC, Oare D, McDowell RS, Burnier JP;
 XX WPI; 2003-553629/52.
 DR Novel variant of atrial natriuretic factor, useful as therapeutic agent
 XX for treating hypertension, congestive heart failure, nephrotic syndrome,
 PT hepatic cirrhosis, pulmonary disease and renal failure.
 XX Disclosure; Col 7; Sipp; English.
 PS The invention relates to an atrial natriuretic factor (ANF, also known as
 XX ANP, a natriuretic peptide) comprising one or more amino acid
 CC substitutions selected from Gly9Thr, Gly9Arg, Gly9Ser, Arg11Asp,
 CC Gly16Arg, Gly16Lys, Gly16Orn, Gly16Har, and Gly16p-amidinophenyl Ala.
 CC Also included is a composition comprising nucleic acid encoding the ANF
 CC variant. The ANF has a decreased binding affinity for the human clearance
 CC receptor. Natriuretic peptide receptor (NPR)-C, compared to wild-type
 CC hANF(1-28) and an equal or higher binding affinity for the human A
 CC receptor, NPR-A, compared to wild-type hANF(1-28). The binding affinity
 CC for NPR-C is less than 50% or 10% of the affinity of wild-type ANF. The
 CC ANF variant has an increased half-life relative to wild-type hANF(1-28)
 CC when incubated with neutral endopeptidase 11.24 (NEP). The ANF variant is
 CC useful for inducing natriuresis, diuresis or vasodilation or inhibit
 CC renin-angiotensin II and aldosterone release and as therapeutic agents in
 CC the treatment of various pathological conditions associated with water or
 CC electrolyte imbalance and hypertension, especially renovascular
 CC hypertension, congestive heart failure (CHF), nephrotic syndrome and
 CC hepatic cirrhosis, pulmonary disease and renal failure due to ineffective
 CC renal perfusion or reduced glomerular filtration rate, to modulate the
 CC activity of other diuretic, natriuretic or vasorelaxant compounds by
 CC binding to alternate receptors, stimulating receptor turnover, or
 CC providing alternate substrates for degradative enzyme of receptor
 CC activity and inhibiting these enzymes or receptors. The present sequence
 CC is the an ANF variant/mutant of the invention.
 XX Sequence 32 AA;
 SQ
 Query Match 100.0%; Score 92; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 DB 10 CFGRKMDRISSSSGLGC 26
 RESULT 44
 ABU63215
 ID ABU63215 standard; peptide; 32 AA.
 AC
 XX ABU63215;
 XX 15-OCT-2003 (first entry)
 XX Human brain natriuretic peptide (BNP).
 DE Natriuretic; renin-suppressing; diuretic; vasodilator; heart failure;
 XX cardiovascular disorder; congestive heart failure; hypertension;
 KW acute kidney failure; chronic kidney failure; liver cirrhosis;
 KW nephrotic syndrome; oedematous state; cardiast; BNP; human;
 KW brain natriuretic peptide.
 XX Homo sapiens.
 OS US2003069186-A1.
 PN 10-APR-2003.
 PT

XX 26-MAR-2002; 2002US-00106806.
 PF 17-DEC-1999; 99US-00466268.
 XX (BURN/) BURNETT J C.
 PA (LISY/) LISY O.
 XX Burnett JC, Lisy O;
 PI WPI; 2003-576433/54.
 DR Novel peptide compound useful for treating or preventing cardiovascular
 XX disorders e.g. congestive heart failure, has natriuretic, renin-
 PT suppressing, diuretic and/or vasodilator activity in mammals.
 XX Disclosure; Fig 1; 43pp; English.
 PS The present invention relates to chimeric peptides having natriuretic,
 CC renin-suppressing, diuretic and/or vasodilator activity in mammals. The
 CC peptides of the invention are useful for treating heart failure in a
 CC mammal e.g. human, rat, mouse, canine, bovine, equine, ovine, caprine or
 CC feline. They are useful for treating and preventing cardiovascular
 CC disorders e.g. congestive heart failure, acute or chronic kidney failure,
 CC hypertension, cirrhosis of liver, nephrotic syndrome and other oedematous
 CC states. The present sequence represents human brain natriuretic peptide
 CC (BNP)
 XX Sequence 32 AA;
 SQ
 Query Match 100.0%; Score 92; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 DB 10 CFGRKMDRISSSSGLGC 26
 RESULT 45
 ADD55931
 ID ADD55931 standard; peptide; 32 AA.
 XX
 AC ADD55931;
 XX 15-JAN-2004 (first entry)
 XX Human B-type natriuretic peptide (BNP).
 DE human; congestive heart failure; CHF; natriuretic peptide;
 KW B-type natriuretic peptide; BNP.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Disulfide-bond 10..26
 FT WO2003079979-A2.
 XX 02-OCT-2003.
 XX 18-MAR-2003; 2003WO-US008215.
 XX 18-MAR-2002; 2002US-0364736P.
 XX (SCIO-) SCIOS INC.
 PA Schreiner GF;
 XX WPI; 2003-767771/72.
 XX Treating congestive heart failure (CHF) in a mammal, comprises
 PT administration of a natriuretic peptide.

XX Disclosure; SEQ ID NO 1; 58pp; English.

XX The invention comprises a method for treating congestive heart failure (CHF), the method involves administering a natriuretic peptide (e.g. human B-type natriuretic peptide). The method is useful for treating congestive heart failure in a mammal that is in a compensated or decompensated state of congestive heart failure. The present amino acid sequence represents the human B-type natriuretic peptide (BNP).

XX Sequence 32 AA;

Query Match 100.0%; Score 92; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 46
ADD93296
ID ADD93296 standard; protein; 32 AA.
AC ADD93296;
XX 29-JAN-2004 (first entry)
XX Human active BNP.
DE
DE
KW prepro; B-type natriuretic peptide; BNP; precursor;
KW cardiac natriuretic peptide; diuretic; vasodilatory; endocrine function;
KW myocyte; heart; congestive heart failure; left ventricle; heart failure;
KW cardiac failure; myocardial infarction;
KW arrhythmogenic right ventricular dysplasia; chronic respiratory disease;
KW tuberculosis; congenital heart disease;
KW obstructive hypertrophic cardiomyopathy; mortality;
KW cardiac related acute dyspnea.
XX
XX Homo sapiens.
XX WO2003087819-A1.
XX 23-OCT-2003.
XX 11-APR-2003; 2003WO-DK000250.
XX 11-APR-2002; 2002AU-00001692.
XX (RIGS-) RIGSHOSPITAL.
XX (UYCO-) UNIV COPENHAGEN.
XX Gotze JP, Rehfeld JF;
XX WPI; 2003-833796/77.
XX Determining the concentration of BNP precursors with antibodies binding to its cleaved product, useful for predicting or diagnosing a cardiac dysfunction, such as congestive heart failure and myocardial infarction.
XX Disclosure; SEQ ID NO 4; 56pp; English.

XX This sequence represents human active B-type natriuretic peptide (BNP).
XX Human BNP is a member of the cardiac natriuretic peptide family. It is 32 amino acids in length with potent natriuretic, diuretic and vasodilatory endocrine functions. It is primarily expressed in the myocytes of the failing heart with BNP increasingly being secreted in to the circulation of patients with congestive heart failure. Increased plasma levels of BNP are associated with impaired function of the left ventricle disregarding the underlying cause and is therefore important in the primary diagnosis of heart failure. The method of the invention for determining the concentration of a BNP precursor, or its fragments, in a sample obtained

CC from a mammal, comprises treating the sample with an agent that cleaves the BNP precursor, and exposing the sample to an antibody that specifically binds to the cleaved product. The elevated level of antibody binding levels in any of the methods cited above is above 15 pmol/L. The methods and compositions of the present invention are useful for predicting or diagnosing a cardiac disease or dysfunction, such as congestive heart failure, impaired function of the left ventricle, cardiac failure after myocardial infarction, arrhythmogenic right ventricular dysplasia, chronic respiratory disease due to tuberculosis, congenital heart disease, obstructive hypertrophic cardiomyopathy, and in predicting mortality in elderly and cardiac related acute dyspnea.

XX Sequence 32 AA;

Query Match 100.0%; Score 92; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 47
ADFI6700
ID ADFI6700 standard; protein; 32 AA.
XX ADFI6700;
XX 12-FEB-2004 (first entry)
XX Human albumin fusion protein-related protein SeqID1802.
DE
XX albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX
XX Homo sapiens.
XX WO2003060071-A2.
XX 24-JUL-2003.
XX 23-DEC-2002; 2002WO-US040891.
XX 21-DEC-2001; 2001US-0341811P.
XX 24-JAN-2002; 2002US-0350358P.
XX 28-JAN-2002; 2002US-0351360P.
XX 26-FEB-2002; 2002US-0359370P.
XX 28-FEB-2002; 2002US-0360000P.
XX 27-MAR-2002; 2002US-0367500P.
XX 08-APR-2002; 2002US-0370227P.
XX 10-MAY-2002; 2002US-0378950P.
XX 24-MAY-2002; 2002US-0382617P.
XX 28-MAY-2002; 2002US-0383123P.
XX 05-JUN-2002; 2002US-0385708P.
XX 10-JUL-2002; 2002US-0394625P.
XX 24-JUL-2002; 2002US-0398008P.
XX 09-AUG-2002; 2002US-0402131P.
XX 13-AUG-2002; 2002US-0402708P.
XX 18-SEP-2002; 2002US-0411355P.
XX 02-OCT-2002; 2002US-0411426P.
XX 11-OCT-2002; 2002US-0417611P.
XX 23-OCT-2002; 2002US-0420246P.
XX 05-NOV-2002; 2002US-0423623P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (DELZ) DELTA BIOTECHNOLOGY LTD.
XX (PRIN-) PRINCIPIA PHARM CORP.
XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX

DR WPI; 2003-598517/56.
DR N-PSDB; ADF16374.
XX
PT New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
PS Example 4; SEQ ID NO 1802; 24pp; English.
XX
CC This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is that of a therapeutic protein
CC which was fused with human albumin to create a novel albumin fusion
CC protein of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 92; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 48
ADJ79634
ID ADJ79634 standard; peptide; 32 AA.
AC ADJ79634;
XX
XX 06-MAY-2004 (first entry)
DT
DE Human Brain Natriuretic Peptide, proBNP(77-108).
XX
XX proBNP(1-108); BNP; Brain Natriuretic Peptide; congestive heart failure;
KW proBNP(77-108).
KW
XX Homo sapiens.
OS
XX WO2004014952-A2.
PN
XX 19-FEB-2004.
PD
XX
XX 07-AUG-2003; 2003WO-FR002483.
PF
XX
XX 07-AUG-2002; 2002FR-00010063.
PR
XX (BIRA) BIO-RAD PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (UYMO-) UNIV MONTPELLIER I.
XX
XX Pau B, Giuliani I, Rieunier F;
PI
XX WPI; 2004-191735/18.
DR
XX New antibodies against pro-brain natriuretic peptide, useful for early
PT diagnosis of congestive heart failure, also new peptides as immunogens.
PT
XX Disclosure; SEQ ID NO 2; 120pp; French.
PS
XX The present invention relates to antibodies directed against proBNP(1-
CC 108) (ADJ79633, where, BNP is Brain Natriuretic Peptide). The antibodies
CC provide a simple and reliable method for early detection of congestive
CC

CC heart failure, suitable for routine use and so are useful for in vitro
CC diagnosis of congestive heart failure in humans. The present sequence is
CC a peptide fragment of proBNP(1-108).
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 92; DB 8; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 49
ADL22384
ID ADL22384 standard; peptide; 32 AA.
XX
AC ADL22384;
XX
XX 20-MAY-2004 (first entry)
DT
DE Natriuretic peptide, SEQ ID No 54.
XX
XX natriuretic peptide; NP; blood; cardiant; hypotensive; antiasthmatic;
KW antiinflammatory; vasotropic; antilipaeamic; nephrotropic;
KW congestive heart failure; hypertension; asthma; inflammation;
KW erectile dysfunction; hypercholesterolaemia; renal disorder.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Residue modified by MPA-AEBA"
FT Disulfide-bond 10. .26
FT Modified-site 32
FT /note= "C-terminal amide"
XX
XX WO2004011498-A2.
PN
XX 05-FEB-2004.
PD
XX
XX 29-JUL-2003; 2003WO-CA001097.
PF
XX
XX 31-JUL-2002; 2002US-0400199P.
PR
XX 31-JUL-2002; 2002US-0400413P.
PR
XX (CONJ-) CONJUCHEM INC.
PA
XX Bridon DP, Bakis P, Carrette J, Leclaire F, Leger R, Robitaille M;
PI WPI; 2004-143823/14.
XX
XX New natriuretic peptide (NP) derivatives having a NP peptide and a
PT reactive entity, useful for the treatment of congestive heart failure,
PT hypertension, asthma, inflammation, hypercholesterolemia and renal
PT disorders.
XX
XX Claim 9; SEQ ID NO 54; 108pp; English.
PS
XX The invention relates to a novel long lasting natriuretic peptide (NP)
CC derivative. The NP derivative comprises an NP peptide, having a 33 amino
CC acid sequence, given in the specification, and a reactive entity coupled
CC to the NP peptide, the reactive entity being capable of covalently
CC bonding with a functionality on a blood component. The NP peptide has an
CC extended in vivo half-life. The natriuretic peptide has the following
CC activities: cardiant, hypotensive, antiasthmatic, antiinflammatory,
CC vasotropic, antilipaeamic, and nephrotropic. The methods and compositions
CC of the present invention are useful for the treatment of congestive heart
CC failure, hypertension, asthma, inflammation, erectile dysfunction, a
CC hypercholesterolaemia and renal disorders. This sequence represents a
CC natriuretic peptide of the invention.

```

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPGKQMDRISSSSGLGC 17
    |||||
Db 10 CPGKQMDRISSSSGLGC 26

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OM protein - protein search, using sw model

Run on: January 25, 2006, 18:46:28 ; Search time 8 Seconds
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23.012 Million cell updates/sec

Title: US-10-737-290-172

Perfect score: 92

Sequence: 1 CPGKWDRISSSLGIC 17

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	92	100.0	27	7	US-11-175-690-322
3	92	100.0	27	7	US-11-175-690-371
4	92	100.0	28	7	US-11-175-690-323
5	92	100.0	28	7	US-11-175-690-369
6	92	100.0	29	7	US-11-175-690-314
7	92	100.0	29	7	US-11-175-690-315
8	92	100.0	32	6	US-10-510-880-4
9	92	100.0	32	6	US-10-977-334-3
10	92	100.0	32	7	US-11-043-590-17
11	92	100.0	32	7	US-11-175-690-288
12	92	100.0	32	7	US-11-175-690-298
13	92	100.0	32	7	US-11-175-690-304
14	92	100.0	32	7	US-11-175-690-317
15	92	100.0	32	7	US-11-175-690-318
16	92	100.0	32	7	US-11-175-690-370
17	92	100.0	42	7	US-11-043-590-15
18	92	100.0	42	7	US-11-175-690-368
19	92	100.0	60	7	US-11-043-590-16
20	92	100.0	108	6	US-10-510-880-5
21	92	100.0	108	6	US-10-875-800-1
22	92	100.0	108	6	US-10-299-977-1
23	92	100.0	134	6	US-10-510-880-1
24	92	100.0	134	6	US-10-875-800-2
25	92	100.0	134	7	US-11-043-590-12
26	92	100.0	134	7	US-11-043-590-12
27	92	100.0	134	7	US-11-043-590-12
28	92	100.0	134	7	US-11-043-590-12
29	92	100.0	134	7	US-11-043-590-12
30	92	100.0	134	7	US-11-043-590-12
31	92	100.0	134	7	US-11-043-590-12
32	92	100.0	134	7	US-11-043-590-12
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27	92	100.0	630	7	US-11-175-690-234	Sequence 234, App
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29	92	100.0	632	7	US-11-175-690-236	Sequence 236, App
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31	92	100.0	641	7	US-11-175-690-211	Sequence 211, App
32	92	100.0	641	7	US-11-175-690-230	Sequence 230, App
33	92	100.0	661	7	US-11-175-690-281	Sequence 281, App
34	92	100.0	663	7	US-11-175-690-284	Sequence 284, App
35	92	100.0	665	7	US-11-175-690-282	Sequence 282, App
36	92	100.0	667	7	US-11-175-690-227	Sequence 227, App
37	92	100.0	670	7	US-11-175-690-283	Sequence 283, App
38	92	100.0	673	7	US-11-175-690-201	Sequence 201, App
39	92	100.0	673	7	US-11-175-690-217	Sequence 217, App
40	92	100.0	673	7	US-11-175-690-231	Sequence 231, App
41	76	82.6	131	6	US-10-510-880-2	Sequence 2, Appli
42	73	79.3	126	6	US-10-977-334-5	Sequence 5, Appli
43	71	77.2	28	7	US-11-112-277-16	Sequence 16, Appl
44	71	77.2	28	7	US-11-112-277-50	Sequence 50, Appl
45	71	77.2	28	7	US-11-112-277-51	Sequence 51, Appl
46	71	77.2	28	7	US-11-059-814-4	Sequence 4, Appli
47	71	77.2	28	7	US-11-175-690-309	Sequence 309, App
48	71	77.2	151	7	US-11-059-814-7	Sequence 7, Appli
49	71	77.2	153	6	US-10-977-334-4	Sequence 4, Appli
50	71	77.2	637	7	US-11-175-690-222	Sequence 222, App
51	67	72.8	152	7	US-11-059-814-16	Sequence 16, Appl
52	65	70.7	121	6	US-10-510-880-3	Sequence 3, Appli
53	43	46.7	85	6	US-10-467-657-3010	Sequence 3010, Ap
54	40.5	44.0	1307	6	US-10-995-561-711	Sequence 711, App
55	40	43.5	593	7	US-11-212-443-64	Sequence 64, Appl
56	40	43.5	4868	7	US-11-044-111-24	Sequence 24, Appl
57	38	41.3	371	6	US-10-821-234-1010	Sequence 1010, Ap
58	38	41.3	761	6	US-10-485-517-252	Sequence 252, App
59	37	40.2	212	7	US-11-044-111-6	Sequence 6, Appli
60	37	40.2	212	7	US-11-044-111-26	Sequence 26, Appl
61	37	40.2	237	7	US-11-044-111-11	Sequence 11, Appl
62	37	40.2	237	7	US-11-044-111-12	Sequence 12, Appl
63	37	40.2	239	7	US-11-044-111-5	Sequence 5, Appli
64	37	40.2	239	7	US-11-044-111-25	Sequence 25, Appl
65	37	40.2	240	7	US-11-044-111-9	Sequence 9, Appli
66	37	40.2	240	7	US-11-044-111-10	Sequence 10, Appl
67	37	40.2	361	6	US-10-838-616-6	Sequence 6, Appli
68	37	40.2	465	6	US-10-467-657-5040	Sequence 5040, Ap
69	37	40.2	508	6	US-10-467-657-7826	Sequence 7826, Ap
70	37	40.2	513	6	US-10-131-826A-536	Sequence 536, App
71	37	40.2	513	6	US-10-063-703-124	Sequence 124, App
72	37	40.2	513	7	US-11-102-240-124	Sequence 124, App
73	37	40.2	585	7	US-11-012-762-6	Sequence 6, Appli
74	37	40.2	1056	7	US-11-044-111-22	Sequence 22, Appl
75	36	39.1	45	6	US-10-957-887B-41	Sequence 41, Appl
76	36	39.1	299	6	US-10-467-657-4424	Sequence 4424, Ap
77	36	39.1	770	6	US-10-821-234-1269	Sequence 1269, Ap
78	35	38.0	144	7	US-11-093-118-14	Sequence 14, Appl
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80	35	38.0	399	7	US-11-018-018-3	Sequence 3, Appli
81	35	38.0	399	7	US-11-047-757-3	Sequence 3, Appli
82	35	38.0	399	7	US-11-166-892-19	Sequence 19, Appl
83	35	38.0	413	6	US-10-467-657-2122	Sequence 2122, Ap
84	35	38.0	558	6	US-10-512-109-11	Sequence 11, Appl
85	34.5	37.5	144	6	US-10-821-234-1255	Sequence 1255, Ap
86	34.5	37.5	500	6	US-10-957-569-18	Sequence 18, Appl
87	34.5	37.5	1963	6	US-10-877-346-43	Sequence 43, Appl
88	34	37.0	43	6	US-10-957-887B-128	Sequence 128, App
89	34	37.0	91	7	US-10-485-788A-818	Sequence 818, App
90	34	37.0	91	7	US-11-053-076-203	Sequence 203, App
91	34	37.0	239	6	US-10-980-388-108	Sequence 108, App
92	34	37.0	315	6	US-10-467-657-4960	Sequence 4960, Ap
93	34	37.0	317	6	US-10-485-517-196	Sequence 196, App
94	34	37.0	335	7	US-11-129-143-106	Sequence 106, App
95	34	37.0	480	6	US-10-467-657-2126	Sequence 2126, Ap
96	34	37.0	550	6	US-10-878-556A-166	Sequence 166, App
97	34	37.0	717	7	US-11-010-239-111	Sequence 111, App
98	34	37.0	719	6	US-10-524-647-116	Sequence 116, App

99	34	37.0	897	6	US-10-336-263A-58	Sequence 58, Appl	172	31.5	34.2	934	7	US-11-077-386-17	Sequence 17, Appl
100	34	37.0	1015	6	US-10-467-657-180	Sequence 180, Appl	173	31.5	34.2	1390	6	US-10-957-351-1	Sequence 1, Appl
101	34	37.0	1015	6	US-10-467-657-3764	Sequence 3764, Ap	174	31.5	34.2	2556	6	US-11-050-346-67	Sequence 67, Appl
102	34	37.0	1059	6	US-10-336-263A-54	Sequence 54, Appl	175		34.2		21	US-10-485-788A-491	Sequence 491, Appl
103	34	37.0	1059	6	US-10-336-263A-56	Sequence 56, Appl	176	31	33.7	29	7	US-11-212-443-147	Sequence 147, Appl
104	34	35.9	42	6	US-10-467-657-614	Sequence 614, Appl	177	31	33.7	115	6	US-10-793-626-1560	Sequence 1560, Ap
105	33	35.9	65	7	US-11-108-841-11	Sequence 11, Appl	178	31	33.7	118	7	US-11-116-144-158	Sequence 158, Appl
106	33	35.9	244	6	US-10-798-579A-22	Sequence 22, Appl	179	31	33.7	160	7	US-11-010-874-12	Sequence 12, Appl
107	33	35.9	415	6	US-10-821-234-936	Sequence 936, App	180	31	33.7	160	7	US-11-055-822-1098	Sequence 1098, Ap
108	33	35.9	513	7	US-11-149-349-6	Sequence 6, Appli	181	31	33.7	168	7	US-11-010-870-7	Sequence 7, Appli
109	33	35.9	592	6	US-10-467-657-4888	Sequence 4888, Ap	182	31	33.7	191	6	US-10-519-390-6	Sequence 6, Appli
110	33	35.9	696	6	US-10-453-372-324	Sequence 324, App	183	31	33.7	191	6	US-10-519-390-23	Sequence 23, Appl
111	33	35.9	696	6	US-10-453-372-336	Sequence 336, App	184	31	33.7	191	6	US-11-033-365-160	Sequence 160, App
112	33	35.9	696	6	US-10-453-372-346	Sequence 346, App	185	31	33.7	192	7	US-11-033-365-159	Sequence 159, App
113	33	35.9	696	6	US-10-453-372-354	Sequence 354, App	186	31	33.7	192	7	US-11-033-365-197	Sequence 197, App
114	33	35.9	696	6	US-10-453-372-356	Sequence 356, App	187	31	33.7	192	7	US-11-033-365-198	Sequence 198, App
115	33	35.9	696	6	US-10-453-372-358	Sequence 358, App	188	31	33.7	192	7	US-11-033-365-200	Sequence 200, App
116	33	35.9	696	6	US-10-453-372-360	Sequence 360, App	189	31	33.7	192	7	US-11-187-522-1	Sequence 1, Appli
117	33	35.9	696	6	US-10-453-372-362	Sequence 362, App	190	31	33.7	193	6	US-10-714-887-360	Sequence 360, App
118	33	35.9	696	6	US-10-453-372-364	Sequence 364, App	191	31	33.7	193	6	US-11-033-365-196	Sequence 196, App
119	33	35.9	696	6	US-10-453-372-366	Sequence 366, App	192	31	33.7	196	7	US-11-033-365-199	Sequence 199, App
120	33	35.9	696	6	US-10-453-372-368	Sequence 368, App	193	31	33.7	201	6	US-10-821-234-1162	Sequence 1162, Ap
121	33	35.9	700	6	US-10-453-372-326	Sequence 326, App	194	31	33.7	202	7	US-11-144-889A-2	Sequence 2, Appli
122	33	35.9	713	6	US-10-453-372-322	Sequence 322, App	195	31	33.7	215	6	US-10-996-007B-27	Sequence 27, Appl
123	33	35.9	757	6	US-10-453-372-320	Sequence 320, App	196	31	33.7	215	7	US-11-074-176-106	Sequence 106, App
124	33	35.9	757	6	US-10-453-372-350	Sequence 350, App	197	31	33.7	251	7	US-11-054-515-1171	Sequence 1171, Ap
125	33	35.9	757	6	US-10-453-372-352	Sequence 352, App	198	31	33.7	260	7	US-11-176-868-12	Sequence 12, Appl
126	33	35.9	763	6	US-10-453-372-328	Sequence 328, App	199	31	33.7	272	7	US-11-000-463-277	Sequence 277, App
127	33	35.9	773	6	US-10-453-372-348	Sequence 348, App	200	31	33.7	286	6	US-10-954-468-25	Sequence 25, Appl
128	33	35.9	778	6	US-10-453-372-330	Sequence 330, App	201	31	33.7	287	6	US-10-954-468-17	Sequence 17, Appl
129	33	35.9	841	6	US-10-453-372-334	Sequence 334, App	202	31	33.7	287	6	US-10-954-468-24	Sequence 24, Appl
130	33	35.9	961	7	US-11-113-424-35	Sequence 35, Appl	203	31	33.7	288	6	US-10-954-468-20	Sequence 22, Appl
131	33	35.9	1554	7	US-11-186-284-93	Sequence 93, Appl	204	31	33.7	288	6	US-10-954-468-22	Sequence 23, Appl
132	33	35.9	2671	6	US-10-876-787-6	Sequence 6, Appli	205	31	33.7	289	6	US-10-954-468-19	Sequence 19, Appl
133	33	35.9	3712	7	US-11-019-711-48	Sequence 48, Appl	206	31	33.7	289	6	US-10-954-468-21	Sequence 21, Appl
134	33	35.9	3712	7	US-11-019-711-51	Sequence 51, Appl	207	31	33.7	290	6	US-10-954-468-18	Sequence 18, Appl
135	33	35.9	5405	7	US-11-108-172-1116	Sequence 1116, Ap	208	31	33.7	291	7	US-11-212-443-138	Sequence 138, App
136	32.5	35.3	49	7	US-11-019-711-57	Sequence 57, Appl	209	31	33.7	292	7	US-11-092-140-32	Sequence 32, Appl
137	32.5	35.3	2766	6	US-10-877-346-62	Sequence 62, Appl	210	31	33.7	293	6	US-10-954-468-14	Sequence 14, Appl
138	32	34.8	117	7	US-11-121-438-30	Sequence 30, Appl	211	31	33.7	302	6	US-10-467-657-5794	Sequence 5794, Ap
139	32	34.8	157	6	US-10-793-626-3268	Sequence 3268, Ap	212	31	33.7	306	7	US-11-153-569-19	Sequence 19, Appl
140	32	34.8	214	7	US-11-128-440-14	Sequence 14, Appl	213	31	33.7	331	6	US-10-467-962B-61	Sequence 61, Appl
141	32	34.8	222	6	US-10-714-887-366	Sequence 366, App	214	31	33.7	331	6	US-11-010-874-2	Sequence 2, Appli
142	32	34.8	266	7	US-11-194-564-65	Sequence 65, Appl	215	31	33.7	339	7	US-11-108-528-62	Sequence 62, Appl
143	32	34.8	310	7	US-11-055-163-9	Sequence 9, Appli	216	31	33.7	359	7	US-11-093-808-7	Sequence 372, App
144	32	34.8	344	6	US-11-055-163-8	Sequence 8, Appli	217	31	33.7	373	6	US-10-793-626-372	Sequence 881, App
145	32	34.8	404	6	US-10-497-135-3	Sequence 3, Appli	218	31	33.7	401	6	US-10-821-234-881	Sequence 383, App
146	32	34.8	404	6	US-10-497-135-4	Sequence 4, Appli	219	31	33.7	408	7	US-11-052-554A-383	Sequence 969, App
147	32	34.8	413	6	US-10-467-657-1858	Sequence 1858, Ap	220	31	33.7	410	6	US-10-995-561-969	Sequence 1, Appli
148	32	34.8	437	6	US-10-131-826A-466	Sequence 466, App	221	31	33.7	412	7	US-11-093-808-1	Sequence 7, Appli
149	32	34.8	510	7	US-11-087-100-26	Sequence 26, Appl	222	31	33.7	412	7	US-11-093-808-8	Sequence 8, Appli
150	32	34.8	510	7	US-11-087-084-26	Sequence 26, Appl	223	31	33.7	412	7	US-11-093-808-9	Sequence 9, Appli
151	32	34.8	510	7	US-11-087-085-26	Sequence 26, Appl	224	31	33.7	412	7	US-11-093-808-10	Sequence 10, Appl
152	32	34.8	514	6	US-10-055-877-226	Sequence 226, App	225	31	33.7	412	7	US-11-093-808-11	Sequence 11, Appl
153	32	34.8	570	7	US-11-113-424-69	Sequence 69, Appl	226	31	33.7	412	7	US-11-093-808-12	Sequence 12, Appl
154	32	34.8	570	7	US-11-113-424-71	Sequence 71, Appl	227	31	33.7	412	7	US-11-093-808-13	Sequence 13, Appl
155	32	34.8	572	6	US-10-878-556A-47	Sequence 47, Appl	228	31	33.7	412	7	US-11-093-808-14	Sequence 14, Appl
156	32	34.8	620	7	US-11-113-424-70	Sequence 70, Appl	229	31	33.7	428	6	US-10-632-150-6	Sequence 6, Appli
157	32	34.8	715	7	US-11-052-554A-290	Sequence 290, App	230	31	33.7	428	7	US-11-073-457-6	Sequence 6, Appli
158	32	34.8	720	7	US-11-113-424-28	Sequence 28, Appl	231	31	33.7	428	7	US-11-073-460-6	Sequence 6, Appli
159	32	34.8	747	7	US-11-113-424-26	Sequence 26, Appl	232	31	33.7	437	7	US-11-088-634A-4	Sequence 4, Appli
160	32	34.8	770	7	US-11-024-959-358	Sequence 358, App	233	31	33.7	444	7	US-11-112-882-15	Sequence 15, Appl
161	32	34.8	794	6	US-10-485-517-355	Sequence 355, App	234	31	33.7	504	7	US-11-087-100-32	Sequence 32, Appl
162	32	34.8	1189	7	US-11-074-176-134	Sequence 134, App	235	31	33.7	504	7	US-11-087-084-32	Sequence 32, Appl
163	32	34.8	2059	7	US-11-087-100-4	Sequence 4, Appli	236	31	33.7	504	7	US-11-087-085-32	Sequence 32, Appl
164	32	34.8	2059	7	US-11-087-084-4	Sequence 4, Appli	237	31	33.7	515	6	US-10-954-468-33	Sequence 33, Appl
165	32	34.8	2059	7	US-11-087-085-4	Sequence 4, Appli	238	31	33.7	515	6	US-10-954-468-32	Sequence 32, Appl
166	32	34.8	2641	6	US-10-877-346-63	Sequence 63, Appl	239	31	33.7	516	6	US-10-954-468-16	Sequence 16, Appl
167	32	34.8	2811	6	US-10-877-346-27	Sequence 27, Appl	240	31	33.7	517	6	US-10-954-468-30	Sequence 30, Appl
168	32	34.8	2814	6	US-10-877-346-25	Sequence 25, Appl	241	31	33.7	518	6	US-10-954-468-13	Sequence 13, Appl
169	31.5	34.2	112	7	US-11-000-463-754	Sequence 754, App	242	31	33.7	520	6	US-10-954-468-13	Sequence 2, Appli
170	31.5	34.2	163	6	US-10-467-657-5884	Sequence 5884, Ap	243	31	33.7	530	7	US-11-088-634A-2	
171	31.5	34.2	906	7	US-11-124-635-4	Sequence 4, Appli	244	31	33.7				

245	31	33.7	542	7	US-11-019-711-97	Sequence 97, Appl	318	30	32.6	344	6	US-10-454-437-148	Sequence 148, App
246	31	33.7	544	7	US-11-159-902-4	Sequence 4, Appl	319	30	32.6	344	6	US-11-055-163-6	Sequence 6, Appl
247	31	33.7	552	7	US-11-052-554A-235	Sequence 235, App	320	30	32.6	350	7	US-10-063-703-8	Sequence 8, Appl
248	31	33.7	592	7	US-11-212-443-6	Sequence 6, Appl	321	30	32.6	350	7	US-11-102-240-8	Sequence 8, Appl
249	31	33.7	592	7	US-11-212-443-91	Sequence 91, Appl	322	30	32.6	354	6	US-10-467-657-6058	Sequence 6058, Ap
250	31	33.7	592	7	US-11-212-443-98	Sequence 98, Appl	323	30	32.6	372	6	US-11-108-528-34	Sequence 34, Appl
251	31	33.7	592	7	US-11-212-443-106	Sequence 106, App	324	30	32.6	382	6	US-10-497-767-2	Sequence 2, Appl
252	31	33.7	592	7	US-11-212-443-107	Sequence 107, App	325	30	32.6	418	6	US-10-467-657-1862	Sequence 1862, Ap
253	31	33.7	592	7	US-11-212-443-110	Sequence 110, App	326	30	32.6	439	7	US-11-075-185-11	Sequence 11, Appl
254	31	33.7	600	7	US-11-212-443-111	Sequence 111, App	327	30	32.6	441	6	US-10-753-537-20	Sequence 20, Appl
255	31	33.7	668	6	US-10-995-561-617	Sequence 619, App	328	30	32.6	458	7	US-11-077-550-114	Sequence 114, App
256	31	33.7	691	6	US-10-995-561-617	Sequence 617, App	329	30	32.6	465	6	US-10-793-626-1676	Sequence 1676, Ap
257	31	33.7	731	7	US-11-052-554A-155	Sequence 155, App	330	30	32.6	472	6	US-10-467-657-86	Sequence 86, Appl
258	31	33.7	742	6	US-10-995-561-615	Sequence 615, App	331	30	32.6	472	6	US-10-467-657-6324	Sequence 6324, Ap
259	31	33.7	742	6	US-10-995-561-618	Sequence 618, App	332	30	32.6	473	6	US-10-131-826A-382	Sequence 382, App
260	31	33.7	756	6	US-10-954-468-15	Sequence 15, Appl	333	30	32.6	483	7	US-11-037-243-79	Sequence 79, Appl
261	31	33.7	756	6	US-10-954-468-27	Sequence 27, Appl	334	30	32.6	514	7	US-11-103-037-3	Sequence 3, Appl
262	31	33.7	758	6	US-10-954-468-28	Sequence 28, Appl	335	30	32.6	515	6	US-10-630-203-6	Sequence 6, Appl
263	31	33.7	759	6	US-10-954-468-12	Sequence 12, Appl	336	30	32.6	515	6	US-11-102-188-3	Sequence 3, Appl
264	31	33.7	759	6	US-10-954-468-26	Sequence 26, Appl	337	30	32.6	522	7	US-11-080-991-104	Sequence 104, App
265	31	33.7	759	6	US-10-954-468-29	Sequence 29, Appl	338	30	32.6	527	7	US-11-010-239-46	Sequence 46, Appl
266	31	33.7	795	6	US-11-052-554A-87	Sequence 87, Appl	339	30	32.6	548	7	US-11-077-550-24	Sequence 24, Appl
267	31	33.7	812	7	US-11-010-874-1	Sequence 1, Appl	340	30	32.6	549	7	US-11-102-188-7	Sequence 7, Appl
268	31	33.7	832	6	US-10-512-109-29	Sequence 29, Appl	341	30	32.6	550	6	US-10-467-657-234	Sequence 234, App
269	31	33.7	833	7	US-11-159-902-2	Sequence 2, Appl	342	30	32.6	550	6	US-10-467-657-924	Sequence 924, App
270	31	33.7	1023	6	US-10-995-561-968	Sequence 968, App	343	30	32.6	561	6	US-10-454-437-330	Sequence 330, App
271	31	33.7	1503	7	US-11-087-100-6	Sequence 6, Appl	344	30	32.6	648	7	US-11-024-959-457	Sequence 457, App
272	31	33.7	1503	7	US-11-087-084-6	Sequence 6, Appl	345	30	32.6	652	7	US-11-079-122-11	Sequence 11, Appl
273	31	33.7	1503	7	US-11-087-085-6	Sequence 6, Appl	346	30	32.6	655	7	US-11-079-122-12	Sequence 12, Appl
274	31	33.7	1591	6	US-10-495-083-4	Sequence 4, Appl	347	30	32.6	655	7	US-11-079-122-13	Sequence 13, Appl
275	31	33.7	1622	6	US-10-495-083-6	Sequence 6, Appl	348	30	32.6	655	7	US-11-079-122-15	Sequence 15, Appl
276	31	33.7	3507	7	US-11-075-185-7	Sequence 7, Appl	349	30	32.6	725	6	US-10-467-657-1536	Sequence 1536, Ap
277	30.5	33.2	112	7	US-11-000-463-282	Sequence 282, App	350	30	32.6	733	7	US-11-012-762-68	Sequence 68, Appl
278	30.5	33.2	416	7	US-11-054-281-137	Sequence 137, App	351	30	32.6	829	6	US-10-512-109-27	Sequence 27, Appl
279	30.5	33.2	416	7	US-11-054-281-138	Sequence 138, App	352	30	32.6	858	7	US-11-077-550-22	Sequence 22, Appl
280	30.5	33.2	502	7	US-11-054-281-140	Sequence 140, App	353	30	32.6	860	7	US-11-077-550-175	Sequence 175, App
281	30.5	33.2	1147	6	US-10-615-668-5	Sequence 5, Appl	354	30	32.6	862	7	US-11-077-550-94	Sequence 94, Appl
282	30	32.6	32	7	US-11-121-301-40	Sequence 40, Appl	355	30	32.6	862	7	US-11-077-550-171	Sequence 171, App
283	30	32.6	32	6	US-10-467-657-1302	Sequence 1302, Ap	356	30	32.6	862	7	US-11-077-550-173	Sequence 173, App
284	30	32.6	37	6	US-10-467-657-7498	Sequence 7498, Ap	357	30	32.6	864	7	US-11-077-550-102	Sequence 102, App
285	30	32.6	39	6	US-10-467-657-1914	Sequence 1914, Ap	358	30	32.6	865	7	US-11-077-550-100	Sequence 100, App
286	30	32.6	71	7	US-11-156-084-94	Sequence 94, Appl	359	30	32.6	866	7	US-11-077-550-88	Sequence 88, Appl
287	30	32.6	118	7	US-11-156-084-57	Sequence 57, Appl	360	30	32.6	866	7	US-11-077-550-104	Sequence 104, App
288	30	32.6	119	7	US-11-073-605-12	Sequence 12, Appl	361	30	32.6	867	7	US-11-077-550-80	Sequence 80, Appl
289	30	32.6	124	6	US-10-467-657-382	Sequence 382, App	362	30	32.6	867	7	US-11-077-550-96	Sequence 96, Appl
290	30	32.6	127	6	US-10-467-657-1320	Sequence 1320, Ap	363	30	32.6	867	7	US-11-077-550-98	Sequence 98, Appl
291	30	32.6	127	6	US-10-467-657-5548	Sequence 5548, Ap	364	30	32.6	870	7	US-11-077-550-92	Sequence 92, Appl
292	30	32.6	127	6	US-10-467-657-7500	Sequence 7500, Ap	365	30	32.6	871	7	US-11-077-550-84	Sequence 84, Appl
293	30	32.6	127	6	US-10-467-657-8260	Sequence 8260, Ap	366	30	32.6	871	7	US-11-077-550-86	Sequence 86, Appl
294	30	32.6	127	6	US-10-467-657-8312	Sequence 8312, Ap	367	30	32.6	871	7	US-11-077-550-90	Sequence 90, Appl
295	30	32.6	132	6	US-10-821-234-1249	Sequence 1248, Ap	368	30	32.6	876	7	US-11-077-550-82	Sequence 82, Appl
296	30	32.6	135	6	US-10-467-657-5364	Sequence 5364, Ap	369	30	32.6	876	7	US-11-077-550-106	Sequence 106, App
297	30	32.6	161	6	US-10-467-657-1786	Sequence 1786, Ap	370	30	32.6	876	7	US-11-077-550-108	Sequence 108, App
298	30	32.6	183	7	US-11-212-443-86	Sequence 86, Appl	371	30	32.6	888	7	US-11-077-550-112	Sequence 112, App
299	30	32.6	208	7	US-11-156-084-97	Sequence 97, Appl	372	30	32.6	915	7	US-11-156-084-119	Sequence 119, App
300	30	32.6	215	7	US-11-202-516-6	Sequence 6, Appl	373	30	32.6	992	7	US-11-010-239-115	Sequence 115, App
301	30	32.6	220	6	US-10-467-657-8734	Sequence 8734, Ap	374	30	32.6	1022	7	US-11-156-084-118	Sequence 118, App
302	30	32.6	232	6	US-10-467-962B-87	Sequence 87, Appl	375	30	32.6	1048	6	US-10-392-234A-20	Sequence 20, Appl
303	30	32.6	240	7	US-11-054-515-1930	Sequence 1930, App	376	30	32.6	1049	7	US-11-069-834-48	Sequence 48, Appl
304	30	32.6	247	7	US-11-054-515-1892	Sequence 1892, Ap	377	30	32.6	1067	7	US-10-392-234A-12	Sequence 12, Appl
305	30	32.6	248	7	US-11-052-554A-56	Sequence 56, App	378	30	32.6	1068	6	US-11/062	Sequence 3, Appl
306	30	32.6	253	7	US-11-054-515-858	Sequence 858, App	379	30	32.6	1092	7	US-11/062	Sequence 6, Appl
307	30	32.6	257	6	US-10-454-437-160	Sequence 160, App	380	30	32.6	1133	6	US-10-821-234-1219	Sequence 20, Appl
308	30	32.6	273	6	US-10-821-234-1203	Sequence 1203, Ap	381	30	32.6	1169	6	US-11-077-550-20	Sequence 20, Appl
309	30	32.6	281	6	US-10-793-626-1026	Sequence 1026, Ap	382	30	32.6	1198	6	US-10-877-346-35	Sequence 35, Appl
310	30	32.6	287	7	US-11-080-991-66	Sequence 66, Appl	383	30	32.6	1327	7	US-11-052-554A-13	Sequence 13, Appl
311	30	32.6	295	7	US-11-194-246-298	Sequence 298, App	384	30	32.6	1389	6	US-10-467-657-334	Sequence 334, App
312	30	32.6	310	7	US-11-055-163-7	Sequence 7, Appl	385	30	32.6	1420	7	US-11-077-550-110	Sequence 110, App
313	30	32.6	329	7	US-11-156-084-28	Sequence 28, Appl	386	30	32.6	1960	7	US-11-069-834-48	Sequence 48, Appl
314	30	32.6	329	7	US-11-156-084-46	Sequence 46, Appl	387	30	32.6	1960	7	US-11-069-834-50	Sequence 50, Appl
315	30	32.6	329	7	US-11-156-084-171	Sequence 171, App	388	30	32.6	2399	7	US-11-052-554A-92	Sequence 92, Appl
316	30	32.6	329	7	US-11-156-084-243	Sequence 243, App	389	30	32.6	3375	7	US-11-044-111-23	Sequence 23, Appl
317	30	32.6	337	6	US-10-821-234-1004	Sequence 1004, Ap	390	29.5	32.1	99	6	US-10-467-657-5934	Sequence 5934, Ap

391	29.5	32.1	112	7	US-11-020-772-10	Sequence 10, Appl	464	29	31.5	342	7	US-11-008-570-45	Sequence 45, Appl
392	29.5	32.1	174	6	US-10-714-887-156	Sequence 156, App	465	29	31.5	353	7	US-11-182-592-4	Sequence 4, Appli
393	29.5	32.1	240	6	US-11-170-653-38	Sequence 38, Appl	466	29	31.5	363	7	US-11-111-239-6	Sequence 6, Appli
394	29.5	32.1	270	6	US-10-793-626-514	Sequence 514, App	467	29	31.5	366	6	US-10-467-657-1164	Sequence 1164, Ap
395	29.5	32.1	336	6	US-10-980-388-120	Sequence 120, App	468	29	31.5	374	7	US-11-051-267-20	Sequence 20, Appl
396	29.5	32.1	683	7	US-11-150-533-26	Sequence 26, Appl	469	29	31.5	393	7	US-11-111-239-8	Sequence 8, Appli
397	29.5	32.1	689	7	US-11-150-533-30	Sequence 30, Appl	470	29	31.5	398	6	US-10-873-528-61	Sequence 61, Appl
398	29.5	32.1	1167	7	US-11-052-554A-121	Sequence 121, App	471	29	31.5	399	7	US-11-111-239-10	Sequence 10, Appl
399	29.5	32.1	2261	6	US-10-995-561-600	Sequence 600, App	472	29	31.5	412	7	US-11-117-161-11	Sequence 11, Appl
400	29.5	32.1	2261	6	US-10-511-545-1	Sequence 1, Appli	473	29	31.5	412	7	US-11-080-257-11	Sequence 11, Appl
401	29.5	32.1	2261	6	US-11-055-309A-9	Sequence 9, Appli	474	29	31.5	434	7	US-11-055-822-794	Sequence 794, App
402	29.5	32.1	2261	7	US-11-055-309A-10	Sequence 10, Appl	475	29	31.5	435	6	US-10-467-657-5694	Sequence 5694, Ap
403	29	31.5	32	7	US-11-046-456-25	Sequence 25, Appl	476	29	31.5	450	7	US-11-087-100-20	Sequence 20, Appl
404	29	31.5	32	7	US-11-046-644-25	Sequence 25, Appl	477	29	31.5	450	7	US-11-087-100-28	Sequence 28, Appl
405	29	31.5	35	7	US-11-046-456-85	Sequence 85, Appl	478	29	31.5	450	7	US-11-087-084-20	Sequence 20, Appl
406	29	31.5	35	7	US-11-046-644-85	Sequence 85, Appl	479	29	31.5	450	7	US-11-087-084-28	Sequence 28, Appl
407	29	31.5	60	7	US-11-046-456-87	Sequence 87, Appl	480	29	31.5	450	7	US-11-087-085-20	Sequence 20, Appl
408	29	31.5	60	7	US-11-046-644-87	Sequence 87, Appl	481	29	31.5	450	7	US-11-087-085-28	Sequence 28, Appl
409	29	31.5	86	6	US-10-485-788A-822	Sequence 822, App	482	29	31.5	454	7	US-11-037-243-103	Sequence 103, App
410	29	31.5	86	7	US-11-053-076-207	Sequence 207, App	483	29	31.5	472	7	US-11-165-211-7	Sequence 7, Appli
411	29	31.5	90	7	US-11-046-456-89	Sequence 89, Appl	484	29	31.5	472	7	US-11-165-226-7	Sequence 7, Appli
412	29	31.5	91	6	US-11-046-644-89	Sequence 89, Appl	485	29	31.5	475	6	US-10-510-386-98	Sequence 98, Appl
413	29	31.5	91	6	US-10-467-657-6622	Sequence 6622, Ap	486	29	31.5	484	6	US-10-763-712A-12	Sequence 12, Appl
414	29	31.5	104	6	US-10-793-626-1880	Sequence 1880, Ap	487	29	31.5	486	6	US-10-467-962B-59	Sequence 59, Appl
415	29	31.5	104	6	US-10-793-626-2200	Sequence 2200, App	488	29	31.5	505	6	US-10-793-626-2220	Sequence 2220, Ap
416	29	31.5	119	7	US-11-124-368A-327	Sequence 327, App	489	29	31.5	505	6	US-10-467-657-6228	Sequence 6228, Ap
417	29	31.5	120	7	US-11-046-456-91	Sequence 91, Appl	490	29	31.5	510	7	US-11-052-554A-119	Sequence 119, App
418	29	31.5	120	7	US-11-046-644-91	Sequence 91, Appl	491	29	31.5	533	7	US-11-128-059-58	Sequence 58, Appl
419	29	31.5	143	6	US-10-821-234-1216	Sequence 1216, Ap	492	29	31.5	557	6	US-10-512-109-9	Sequence 9, Appli
420	29	31.5	143	6	US-10-821-234-1084	Sequence 1084, Ap	493	29	31.5	567	6	US-10-995-561-764	Sequence 764, App
421	29	31.5	150	7	US-11-046-456-93	Sequence 93, Appl	494	29	31.5	572	7	US-11-043-889-13	Sequence 13, Appl
422	29	31.5	150	7	US-11-046-644-93	Sequence 93, Appl	495	29	31.5	574	6	US-10-517-939-108	Sequence 108, App
423	29	31.5	151	6	US-10-821-234-1524	Sequence 1524, Ap	496	29	31.5	703	6	US-10-821-234-1412	Sequence 1412, Ap
424	29	31.5	151	6	US-10-821-234-1333	Sequence 133, App	497	29	31.5	704	6	US-10-505-263-10	Sequence 10, Appl
425	29	31.5	160	7	US-11-010-874-13	Sequence 13, Appl	498	29	31.5	746	7	US-11-024-959-346	Sequence 346, App
426	29	31.5	160	7	US-11-010-874-14	Sequence 14, Appl	499	29	31.5	746	6	US-10-793-626-138	Sequence 138, App
427	29	31.5	160	7	US-11-044-285-4	Sequence 4, Appli	500	29	31.5	751	6	US-10-467-657-1418	Sequence 1418, Ap
428	29	31.5	168	7	US-11-010-874-8	Sequence 8, Appli	501	29	31.5	791	7	US-11-056-621-4	Sequence 4, Appli
429	29	31.5	168	7	US-11-010-874-9	Sequence 9, Appli	502	29	31.5	810	6	US-10-995-561-761	Sequence 761, App
430	29	31.5	176	7	US-11-052-554A-39	Sequence 39, Appl	503	29	31.5	810	6	US-10-220-824-2	Sequence 2, Appli
431	29	31.5	180	7	US-11-046-456-95	Sequence 95, Appl	504	29	31.5	817	6	US-10-453-372-520	Sequence 520, App
432	29	31.5	180	7	US-11-046-644-95	Sequence 95, Appl	505	29	31.5	825	7	US-11-074-176-20	Sequence 20, Appl
433	29	31.5	204	6	US-10-467-657-2696	Sequence 2696, Ap	506	29	31.5	1048	6	US-10-392-234A-14	Sequence 14, Appl
434	29	31.5	204	6	US-10-467-657-6710	Sequence 6710, App	507	29	31.5	1048	6	US-10-392-234A-18	Sequence 18, Appl
435	29	31.5	210	7	US-11-046-456-97	Sequence 97, App	508	29	31.5	1061	7	US-11-000-463-347	Sequence 347, App
436	29	31.5	210	7	US-11-046-644-97	Sequence 97, Appl	509	29	31.5	1076	6	US-10-467-657-5708	Sequence 5708, Ap
437	29	31.5	217	6	US-10-467-657-8174	Sequence 8174, Ap	510	29	31.5	1081	7	US-11-113-751-38	Sequence 38, Appl
438	29	31.5	224	6	US-10-793-626-1430	Sequence 1430, Ap	511	29	31.5	1083	7	US-11-113-751-40	Sequence 40, Appl
439	29	31.5	240	7	US-11-082-389-82	Sequence 82, Appl	512	29	31.5	1091	7	US-11-000-463-348	Sequence 348, App
440	29	31.5	243	7	US-11-046-456-10	Sequence 10, Appl	513	29	31.5	1116	7	US-11-113-751-32	Sequence 32, Appl
441	29	31.5	243	7	US-11-046-456-180	Sequence 180, App	514	29	31.5	1116	7	US-11-113-751-34	Sequence 34, Appl
442	29	31.5	243	7	US-11-046-644-10	Sequence 10, Appl	515	29	31.5	1118	7	US-11-113-751-42	Sequence 42, Appl
443	29	31.5	245	6	US-10-055-877-196	Sequence 196, App	516	29	31.5	1121	7	US-11-113-751-19	Sequence 19, Appl
444	29	31.5	245	7	US-11-046-456-69	Sequence 69, Appl	517	29	31.5	1151	7	US-11-113-751-36	Sequence 36, Appl
445	29	31.5	245	7	US-11-046-644-69	Sequence 69, Appl	518	29	31.5	1153	7	US-11-113-751-44	Sequence 44, Appl
446	29	31.5	263	7	US-11-046-456-4	Sequence 4, Appli	519	29	31.5	1346	7	US-11-060-005-2	Sequence 2, Appli
447	29	31.5	263	7	US-11-046-456-179	Sequence 179, App	520	29	31.5	1416	7	US-11-128-059-60	Sequence 60, Appl
448	29	31.5	263	7	US-11-046-644-4	Sequence 4, Appli	521	29	31.5	1494	7	US-11-128-059-78	Sequence 78, Appl
449	29	31.5	264	6	US-10-467-657-6940	Sequence 6940, Ap	522	29	31.5	1496	7	US-11-186-284-35	Sequence 35, Appl
450	29	31.5	279	6	US-10-055-877-197	Sequence 197, App	523	29	31.5	1579	7	US-11-052-554A-9	Sequence 9, Appli
451	29	31.5	285	7	US-11-429-143-185	Sequence 185, App	524	29	31.5	1596	7	US-11-060-005-4	Sequence 4, Appli
452	29	31.5	302	5	US-09-978-360A-407	Sequence 407, App	525	29	31.5	1663	6	US-10-982-545-6	Sequence 6, Appli
453	29	31.5	302	7	US-11-182-592-6	Sequence 6, Appli	526	29	31.5	1786	7	US-11-196-400-3	Sequence 3, Appli
454	29	31.5	308	6	US-10-131-826A-100	Sequence 100, App	527	29	31.5	2086	7	US-11-128-059-82	Sequence 82, Appl
455	29	31.5	308	7	US-11-046-456-6	Sequence 6, Appli	528	29	31.5	2096	6	US-10-995-561-606	Sequence 606, App
456	29	31.5	308	7	US-11-046-644-6	Sequence 6, Appli	529	29	31.5	2197	7	US-11-075-185-8	Sequence 8, Appli
457	29	31.5	308	7	US-11-052-554A-251	Sequence 251, App	530	29	31.5	2313	6	US-11-128-059-80	Sequence 80, Appl
458	29	31.5	310	6	US-10-454-437-328	Sequence 328, App	531	29	31.5	2351	6	US-10-995-561-608	Sequence 608, App
459	29	31.5	329	6	US-10-467-657-2240	Sequence 2240, Ap	532	29	31.5	2358	7	US-11-128-059-74	Sequence 74, Appl
460	29	31.5	333	6	US-10-878-556A-174	Sequence 174, App	533	29	31.5	2417	6	US-10-453-372-228	Sequence 228, App
461	29	31.5	338	6	US-10-467-657-3178	Sequence 3178, Ap	534	29	31.5	2439	7	US-11-128-059-76	Sequence 76, Appl
462	29	31.5	339	7	US-11-010-874-3	Sequence 3, Appli	535	29	31.5	2458	7	US-11-128-059-94	Sequence 94, Appl
463	29	31.5	339	7	US-11-010-874-4	Sequence 4, Appli	536	29	31.5	2551	6	US-10-453-372-256	Sequence 256, App

537	29	31.5	2551	7	US-11-128-059-96	Sequence 96, Appl	610	28	30.4	321	7	US-11-212-443-10	Sequence 10, Appl
538	29	31.5	2902	7	US-11-052-554A-91	Sequence 91, Appl	611	28	30.4	321	7	US-11-212-443-12	Sequence 12, Appl
539	28.5	31.0	35	6	US-10-957-351-120	Sequence 120, Appl	612	28	30.4	322	6	US-10-467-657-1006	Sequence 1006, Ap
540	28.5	31.0	181	7	US-11-175-690-344	Sequence 344, Appl	613	28	30.4	322	6	US-10-055-877-26	Sequence 26, Appl
541	28.5	31.0	181	7	US-11-175-690-345	Sequence 345, Appl	614	28	30.4	324	6	US-10-467-657-722	Sequence 722, Appl
542	28.5	31.0	181	7	US-11-175-690-346	Sequence 346, Appl	615	28	30.4	327	6	US-10-793-626-1104	Sequence 1104, Ap
543	28.5	31.0	181	7	US-11-175-690-347	Sequence 347, Appl	616	28	30.4	327	6	US-10-793-626-1104	Sequence 1104, Ap
544	28.5	31.0	181	7	US-11-175-690-348	Sequence 348, Appl	617	28	30.4	335	6	US-10-873-528-4	Sequence 4, Appl
545	28.5	31.0	181	7	US-11-175-690-349	Sequence 349, Appl	618	28	30.4	336	7	US-11-129-143-105	Sequence 105, App
546	28.5	31.0	238	6	US-10-927-641-68	Sequence 68, Appl	619	28	30.4	341	6	US-10-821-234-1628	Sequence 1628, Ap
547	28.5	31.0	344	6	US-10-967-527A-24	Sequence 24, Appl	620	28	30.4	344	6	US-10-995-561-740	Sequence 740, App
548	28.5	31.0	362	6	US-10-467-657-6880	Sequence 6880, Ap	621	28	30.4	344	6	US-10-995-561-744	Sequence 744, App
549	28.5	31.0	415	7	US-11-055-822-816	Sequence 816, App	622	28	30.4	344	7	US-11-008-570-44	Sequence 44, Appl
550	28.5	31.0	437	7	US-11-194-246-324	Sequence 324, App	623	28	30.4	350	6	US-10-467-657-1972	Sequence 1972, Ap
551	28.5	31.0	442	7	US-11-055-822-814	Sequence 814, App	624	28	30.4	351	6	US-10-467-657-8316	Sequence 8316, Ap
552	28.5	31.0	491	6	US-10-763-712A-4	Sequence 4, Appli	625	28	30.4	351	6	US-10-838-616-22	Sequence 22, Appl
553	28.5	31.0	500	6	US-10-467-657-594	Sequence 594, App	626	28	30.4	357	7	US-11-108-528-60	Sequence 60, Appl
554	28.5	31.0	790	7	US-11-175-690-257	Sequence 257, App	627	28	30.4	358	6	US-10-467-657-6970	Sequence 6970, Ap
555	28.5	31.0	790	7	US-11-175-690-258	Sequence 258, App	628	28	30.4	360	7	US-11-108-528-6	Sequence 6, Appli
556	28.5	31.0	790	7	US-11-175-690-259	Sequence 259, App	629	28	30.4	363	6	US-10-055-877-14	Sequence 14, Appl
557	28.5	31.0	790	7	US-11-175-690-260	Sequence 260, App	630	28	30.4	363	7	US-11-055-822-646	Sequence 646, App
558	28.5	31.0	790	7	US-11-175-690-261	Sequence 261, App	631	28	30.4	364	6	US-10-877-346-64	Sequence 64, Appl
559	28.5	31.0	790	7	US-11-175-690-262	Sequence 262, App	632	28	30.4	374	6	US-10-055-877-20	Sequence 20, Appl
560	28.5	31.0	4655	6	US-10-995-561-556	Sequence 556, App	633	28	30.4	374	6	US-10-055-877-22	Sequence 22, Appl
561	28	30.4	21	6	US-10-893-584-205	Sequence 205, App	634	28	30.4	374	7	US-11-037-243-61	Sequence 61, Appl
562	28	30.4	39	6	US-10-467-657-3574	Sequence 3574, Ap	635	28	30.4	381	6	US-10-454-437-316	Sequence 316, App
563	28	30.4	41	7	US-11-043-788-492	Sequence 492, App	636	28	30.4	387	6	US-10-467-657-5522	Sequence 5522, Ap
564	28	30.4	43	6	US-10-957-887B-73	Sequence 73, Appl	637	28	30.4	389	7	US-11-019-711-131	Sequence 131, App
565	28	30.4	44	6	US-10-957-887B-209	Sequence 209, App	638	28	30.4	391	6	US-10-878-556A-86	Sequence 86, Appl
566	28	30.4	44	6	US-10-957-887B-251	Sequence 251, App	639	28	30.4	391	6	US-10-995-561-739	Sequence 739, App
567	28	30.4	66	6	US-10-467-657-766	Sequence 766, App	640	28	30.4	398	7	US-11-130-391-1	Sequence 1, Appli
568	28	30.4	75	6	US-10-467-657-4938	Sequence 4938, Ap	641	28	30.4	398	7	US-11-130-391-2	Sequence 2, Appli
569	28	30.4	76	6	US-10-995-561-591	Sequence 591, App	642	28	30.4	398	7	US-11-129-574-1	Sequence 1, Appli
570	28	30.4	76	6	US-10-995-561-592	Sequence 592, App	643	28	30.4	398	7	US-11-129-574-2	Sequence 2, Appli
571	28	30.4	79	7	US-11-077-386-21	Sequence 21, Appl	644	28	30.4	399	6	US-10-467-657-7478	Sequence 7478, Ap
572	28	30.4	89	6	US-10-467-657-3582	Sequence 3582, Ap	645	28	30.4	404	7	US-11-052-554A-344	Sequence 344, App
573	28	30.4	92	6	US-10-485-788A-758	Sequence 758, App	646	28	30.4	425	6	US-10-336-263A-2	Sequence 2, Appli
574	28	30.4	92	7	US-11-053-076-135	Sequence 135, App	647	28	30.4	429	6	US-10-523-038-48	Sequence 48, Appl
575	28	30.4	100	7	US-11-025-712-7	Sequence 7, Appli	648	28	30.4	429	6	US-11-129-442-40	Sequence 40, Appl
576	28	30.4	101	6	US-10-793-626-3002	Sequence 3002, Ap	649	28	30.4	430	6	US-10-517-939-80	Sequence 80, Appl
577	28	30.4	102	6	US-10-485-788A-783	Sequence 783, App	650	28	30.4	432	6	US-10-821-234-1463	Sequence 1463, Ap
578	28	30.4	102	7	US-11-053-076-165	Sequence 165, App	651	28	30.4	432	6	US-10-995-561-738	Sequence 738, App
579	28	30.4	115	6	US-10-793-626-1150	Sequence 1150, Ap	652	28	30.4	438	6	US-10-877-346-58	Sequence 58, Appl
580	28	30.4	129	6	US-10-501-039-8	Sequence 8, Appli	653	28	30.4	438	6	US-10-877-346-59	Sequence 59, Appl
581	28	30.4	130	7	US-11-194-246-415	Sequence 415, App	654	28	30.4	441	7	US-11-024-959-410	Sequence 410, App
582	28	30.4	185	6	US-10-467-657-1228	Sequence 1228, Ap	655	28	30.4	445	6	US-10-995-561-746	Sequence 746, App
583	28	30.4	191	7	US-11-151-601-38	Sequence 38, Appl	656	28	30.4	448	7	US-11-052-554A-65	Sequence 65, Appl
584	28	30.4	196	7	US-11-093-118-35	Sequence 35, Appl	657	28	30.4	457	6	US-10-995-561-741	Sequence 741, App
585	28	30.4	197	6	US-10-714-887-98	Sequence 98, Appl	658	28	30.4	459	7	US-11-024-959-299	Sequence 299, App
586	28	30.4	198	7	US-11-043-788-195	Sequence 195, App	659	28	30.4	461	7	US-11-082-389-176	Sequence 176, App
587	28	30.4	206	6	US-10-467-657-3004	Sequence 3004, Ap	660	28	30.4	491	6	US-10-995-561-743	Sequence 743, App
588	28	30.4	210	6	US-10-055-877-24	Sequence 24, Appl	661	28	30.4	492	6	US-10-524-647-130	Sequence 130, App
589	28	30.4	210	7	US-11-052-554A-328	Sequence 328, App	662	28	30.4	495	7	US-11-052-554A-258	Sequence 258, App
590	28	30.4	228	6	US-10-714-887-90	Sequence 90, Appl	663	28	30.4	503	6	US-10-873-528-74	Sequence 74, Appl
591	28	30.4	229	6	US-10-467-657-6238	Sequence 6238, Ap	664	28	30.4	508	7	US-11-075-185-26	Sequence 26, Appl
592	28	30.4	240	7	US-11-212-443-139	Sequence 139, App	665	28	30.4	512	6	US-10-995-561-745	Sequence 745, App
593	28	30.4	240	7	US-11-212-443-159	Sequence 159, App	666	28	30.4	512	6	US-10-517-939-236	Sequence 236, App
594	28	30.4	252	6	US-10-527-500-19	Sequence 19, Appl	667	28	30.4	512	7	US-11-010-239-69	Sequence 69, Appl
595	28	30.4	253	7	US-11-054-515-1095	Sequence 1095, Ap	668	28	30.4	514	6	US-10-821-234-998	Sequence 998, App
596	28	30.4	254	6	US-10-821-234-980	Sequence 980, App	669	28	30.4	522	6	US-10-995-561-1030	Sequence 1030, Ap
597	28	30.4	263	7	US-11-046-644-18	Sequence 18, Appl	670	28	30.4	527	7	US-11-052-554A-304	Sequence 304, App
598	28	30.4	267	7	US-11-165-067A-3	Sequence 3, Appli	671	28	30.4	536	6	US-10-714-887-256	Sequence 256, App
599	28	30.4	257	7	US-11-054-515-1531	Sequence 1531, Ap	672	28	30.4	537	7	US-11-129-442-47	Sequence 47, Appl
600	28	30.4	259	6	US-10-821-234-1561	Sequence 1561, Ap	673	28	30.4	550	7	US-11-043-889-5	Sequence 5, Appli
601	28	30.4	259	6	US-10-467-657-3410	Sequence 3410, Ap	674	28	30.4	579	7	US-11-045-802-32	Sequence 32, Appl
602	28	30.4	263	7	US-11-046-456-18	Sequence 18, Appl	675	28	30.4	596	7	US-11-152-903-2	Sequence 2, Appli
603	28	30.4	267	7	US-11-165-067A-3	Sequence 3, Appli	676	28	30.4	596	7	US-11-152-903-6	Sequence 6, Appli
604	28	30.4	267	7	US-11-165-067A-3	Sequence 3, Appli	677	28	30.4	596	7	US-11-152-903-8	Sequence 8, Appli
605	28	30.4	270	6	US-10-467-657-5426	Sequence 5426, Ap	678	28	30.4	596	7	US-11-152-903-10	Sequence 10, Appl
606	28	30.4	271	7	US-11-179-977-10	Sequence 10, Appl	679	28	30.4	596	7	US-11-152-903-12	Sequence 12, Appl
607	28	30.4	278	7	US-11-055-822-984	Sequence 984, App	680	28	30.4	601	6	US-11-467-657-7120	Sequence 7120, Ap
608	28	30.4	280	7	US-11-170-653-66	Sequence 66, Appl	681	28	30.4	601	6	US-11-467-657-7120	Sequence 7120, Ap
609	28	30.4	318	7	US-11-016-564-8	Sequence 8, Appli	682	28	30.4	630	7	US-11-196-400-5	Sequence 5, Appli

683	28	30.4	639	6	US-10-821-234-907	Sequence 907, App	756	27	29.3	29	7	US-11-089-601-20	Sequence 20, Appl
684	28	30.4	644	6	US-10-821-234-1107	Sequence 1107, Ap	757	27	29.3	29	7	US-11-089-601-21	Sequence 21, Appl
685	28	30.4	645	6	US-10-763-712A-17	Sequence 17, Appl	758	27	29.3	37	6	US-10-467-657-1648	Sequence 1648, Ap
686	28	30.4	645	6	US-10-763-712A-105	Sequence 105, App	759	27	29.3	39	7	US-11-068-783-106	Sequence 106, App
687	28	30.4	660	6	US-10-878-556A-105	Sequence 102, App	760	27	29.3	43	6	US-10-957-887B-223	Sequence 223, App
688	28	30.4	669	7	US-11-024-959-520	Sequence 520, App	761	27	29.3	43	6	US-10-957-887B-234	Sequence 234, App
689	28	30.4	708	7	US-11-196-475-76	Sequence 76, Appl	762	27	29.3	49	6	US-10-467-657-3008	Sequence 3008, Ap
690	28	30.4	726	7	US-11-124-368A-247	Sequence 247, App	763	27	29.3	66	6	US-10-467-657-6624	Sequence 6624, Ap
691	28	30.4	729	7	US-11-099-691-3	Sequence 3, Appli	764	27	29.3	73	7	US-11-051-481-27	Sequence 27, Appl
692	28	30.4	732	7	US-11-124-368A-248	Sequence 248, App	765	27	29.3	78	6	US-10-485-788A-692	Sequence 692, App
693	28	30.4	740	6	US-10-821-234-1464	Sequence 1464, Ap	766	27	29.3	78	7	US-11-053-076-62	Sequence 62, Appl
694	28	30.4	753	7	US-11-037-243-68	Sequence 68, Appl	767	27	29.3	85	6	US-10-925-366A-350	Sequence 350, App
695	28	30.4	780	7	US-11-089-551A-22	Sequence 22, Appl	768	27	29.3	86	6	US-10-925-366A-357	Sequence 357, App
696	28	30.4	795	6	US-10-821-234-1002	Sequence 1002, Ap	769	27	29.3	87	7	US-11-051-481-26	Sequence 26, Appl
697	28	30.4	801	6	US-10-793-626-2030	Sequence 2020, Ap	770	27	29.3	89	6	US-10-925-366A-367	Sequence 367, App
698	28	30.4	803	7	US-11-124-368A-241	Sequence 241, App	771	27	29.3	92	6	US-10-667-295-108	Sequence 108, App
699	28	30.4	803	7	US-11-124-368A-242	Sequence 242, App	772	27	29.3	92	6	US-10-667-295-134	Sequence 134, App
700	28	30.4	805	7	US-10-927-641-77	Sequence 77, Appl	773	27	29.3	97	7	US-11-075-351-59	Sequence 59, Appl
701	28	30.4	844	6	US-10-763-712A-48	Sequence 48, Appl	774	27	29.3	97	7	US-11-093-274-34	Sequence 34, Appl
702	28	30.4	875	7	US-11-024-959-352	Sequence 352, App	775	27	29.3	98	6	US-10-789-273-10	Sequence 10, Appl
703	28	30.4	896	6	US-10-467-657-7004	Sequence 7004, Ap	776	27	29.3	98	7	US-11-144-248-32	Sequence 32, Appl
704	28	30.4	914	6	US-10-312-954-2	Sequence 2, Appli	777	27	29.3	98	7	US-11-054-669-22	Sequence 22, Appl
705	28	30.4	915	6	US-10-647-956A-6	Sequence 6, Appli	778	27	29.3	98	7	US-11-084-554-33	Sequence 33, Appl
706	28	30.4	943	6	US-10-821-234-1012	Sequence 1012, Ap	779	27	29.3	98	7	US-11-144-222-32	Sequence 32, Appl
707	28	30.4	944	7	US-11-057-058-68	Sequence 68, Appl	780	27	29.3	98	7	US-11-004-590-23	Sequence 23, Appl
708	28	30.4	1029	6	US-10-821-234-908	Sequence 908, App	781	27	29.3	100	6	US-10-467-657-9162	Sequence 9162, Ap
709	28	30.4	1061	7	US-11-121-438-4	Sequence 4, Appli	782	27	29.3	109	7	US-11-053-076-20	Sequence 20, Appl
710	28	30.4	1065	7	US-11-191-374-16	Sequence 16, Appl	783	27	29.3	115	6	US-10-467-657-2032	Sequence 2032, Ap
711	28	30.4	1065	7	US-11-191-375-16	Sequence 16, Appl	784	27	29.3	116	6	US-10-925-366A-1	Sequence 1, Appli
712	28	30.4	1065	7	US-11-191-588-16	Sequence 16, Appl	785	27	29.3	118	6	US-10-771-257-8	Sequence 8, Appli
713	28	30.4	1069	7	US-11-191-374-17	Sequence 17, Appl	786	27	29.3	118	7	US-11-127-677-8	Sequence 8, Appli
714	28	30.4	1069	7	US-11-191-375-17	Sequence 17, Appl	787	27	29.3	118	7	US-11-112-240-22	Sequence 22, Appl
715	28	30.4	1069	7	US-11-191-588-17	Sequence 17, Appl	788	27	29.3	118	7	US-11-112-304A-22	Sequence 22, Appl
716	28	30.4	1073	6	US-10-467-657-5230	Sequence 5230, Ap	789	27	29.3	119	6	US-10-485-788A-770	Sequence 770, App
717	28	30.4	1110	7	US-11-113-751-4	Sequence 4, Appli	790	27	29.3	119	6	US-10-771-257-10	Sequence 10, Appl
718	28	30.4	1268	7	US-11-052-554B-1	Sequence 1, Appli	791	27	29.3	119	7	US-11-053-076-147	Sequence 147, App
719	28	30.4	1450	6	US-10-485-517-152	Sequence 152, App	792	27	29.3	119	7	US-11-127-677-10	Sequence 10, Appl
720	28	30.4	1463	6	US-10-971-982-3	Sequence 3, Appli	793	27	29.3	120	6	US-10-793-626-2404	Sequence 2404, Ap
721	28	30.4	1544	6	US-10-453-372-1186	Sequence 1186, Ap	794	27	29.3	120	6	US-10-925-366A-235	Sequence 235, App
722	28	30.4	1565	6	US-10-453-372-1180	Sequence 1180, Ap	795	27	29.3	120	6	US-10-925-366A-286	Sequence 286, App
723	28	30.4	1566	6	US-10-453-372-1190	Sequence 1190, Ap	796	27	29.3	120	6	US-10-834-397-38	Sequence 38, Appl
724	28	30.4	1588	7	US-11-043-889-37	Sequence 37, Appl	797	27	29.3	120	6	US-10-834-397-63	Sequence 2, Appli
725	28	30.4	1627	6	US-10-821-234-1283	Sequence 1283, Ap	798	27	29.3	120	7	US-11-112-240-2	Sequence 2, Appli
726	28	30.4	2053	6	US-10-453-372-1174	Sequence 1174, Ap	799	27	29.3	121	6	US-11-112-304A-2	Sequence 2, Appli
727	28	30.4	2143	6	US-10-453-372-1188	Sequence 1188, Ap	800	27	29.3	121	6	US-10-789-273-9	Sequence 9, Appli
728	28	30.4	2314	7	US-11-013-759-11	Sequence 11, Appl	801	27	29.3	121	7	US-10-771-257-7	Sequence 7, Appli
729	28	30.4	3635	7	US-11-019-711-47	Sequence 47, Appl	802	27	29.3	121	7	US-11-074-176-86	Sequence 86, Appl
730	27.5	29.9	103	6	US-10-467-657-6846	Sequence 6846, Ap	803	27	29.3	121	7	US-11-127-677-7	Sequence 7, Appli
731	27.5	29.9	109	6	US-10-467-657-7852	Sequence 7852, Ap	804	27	29.3	122	7	US-11-112-240-6	Sequence 6, Appli
732	27.5	29.9	119	6	US-10-467-657-6848	Sequence 6848, Ap	805	27	29.3	122	7	US-11-112-304A-6	Sequence 6, Appli
733	27.5	29.9	162	7	US-11-024-959-441	Sequence 441, App	806	27	29.3	123	6	US-10-925-366A-216	Sequence 216, App
734	27.5	29.9	189	6	US-10-416-384-1	Sequence 1, Appli	807	27	29.3	123	7	US-11-112-240-30	Sequence 30, Appl
735	27.5	29.9	349	7	US-11-108-528-44	Sequence 44, Appl	808	27	29.3	123	6	US-11-112-304A-30	Sequence 30, Appl
736	27.5	29.9	356	7	US-11-143-986-8	Sequence 8, Appli	809	27	29.3	124	6	US-10-771-257-22	Sequence 22, Appl
737	27.5	29.9	356	7	US-11-143-986-9	Sequence 9, Appli	810	27	29.3	124	7	US-11-144-248-8	Sequence 8, Appli
738	27.5	29.9	430	6	US-10-821-234-1437	Sequence 1437, Ap	811	27	29.3	124	7	US-11-127-677-22	Sequence 22, Appl
739	27.5	29.9	497	7	US-11-037-829A-15	Sequence 15, Appl	812	27	29.3	124	7	US-11-144-222-8	Sequence 8, Appli
740	27.5	29.9	500	6	US-10-467-657-105	Sequence 105, App	813	27	29.3	125	6	US-10-771-257-43	Sequence 43, Appl
741	27.5	29.9	841	6	US-10-770-726-88	Sequence 88, Appl	814	27	29.3	125	7	US-11-144-248-16	Sequence 16, Appl
742	27.5	29.9	1031	6	US-10-857-780-22	Sequence 22, Appl	815	27	29.3	125	7	US-11-127-677-41	Sequence 41, Appl
743	27.5	29.9	1114	6	US-10-857-780-27	Sequence 27, Appl	816	27	29.3	125	7	US-11-144-222-16	Sequence 16, Appl
744	27.5	29.9	1377	6	US-10-467-657-7922	Sequence 7922, Ap	817	27	29.3	126	6	US-10-771-257-13	Sequence 13, Appl
745	27.5	29.9	1732	6	US-10-055-877-147	Sequence 147, App	818	27	29.3	126	7	US-11-127-677-13	Sequence 13, Appl
746	27	29.3	16	7	US-11-089-764-4	Sequence 4, Appli	819	27	29.3	127	7	US-11-116-144-91	Sequence 91, Appl
747	27	29.3	25	7	US-11-089-601-15	Sequence 15, Appl	820	27	29.3	129	6	US-10-793-626-2138	Sequence 2138, Ap
748	27	29.3	28	7	US-11-089-601-22	Sequence 22, Appl	821	27	29.3	130	6	US-10-507-275-1	Sequence 1, Appli
749	27	29.3	29	7	US-11-089-601-2	Sequence 2, Appli	822	27	29.3	130	7	US-11-109-264-51	Sequence 51, Appl
750	27	29.3	29	7	US-11-089-601-10	Sequence 10, Appl	823	27	29.3	130	7	US-11-109-264-52	Sequence 52, Appl
751	27	29.3	29	7	US-11-089-601-11	Sequence 11, Appl	824	27	29.3	130	7	US-11-109-264-53	Sequence 53, Appl
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753	27	29.3	29	7	US-11-089-601-14	Sequence 14, Appl	826	27	29.3	130	7	US-11-116-144-121	Sequence 121, App
754	27	29.3	29	7	US-11-089-601-17	Sequence 17, Appl	827	27	29.3	131	7	US-11-084-591-3	Sequence 3, Appli
755	27	29.3	29	7	US-11-089-601-19	Sequence 19, Appl	828	27	29.3	134	6	US-10-467-657-5072	Sequence 5072, Ap

829	27	29.3	138	7	US-11-080-991-12	Sequence 12, Appl	902	27	29.3	250	6	US-10-131-826A-78	Sequence 78, Appl
830	27	29.3	139	6	US-10-721-763-33	Sequence 33, Appl	903	27	29.3	250	7	US-11-054-515-1420	Sequence 1420, Ap
831	27	29.3	142	6	US-10-789-273-16	Sequence 16, Appl	904	27	29.3	250	7	US-11-054-515-1461	Sequence 1461, Ap
832	27	29.3	146	7	US-11-074-176-280	Sequence 280, App	905	27	29.3	251	7	US-11-054-515-908	Sequence 908, App
833	27	29.3	166	6	US-10-467-657-198	Sequence 198, App	906	27	29.3	251	7	US-11-054-515-1708	Sequence 1708, Ap
834	27	29.3	166	7	US-11-132-722-45	Sequence 45, Appl	907	27	29.3	251	7	US-11-054-515-1740	Sequence 1740, Ap
835	27	29.3	166	7	US-11-175-690-104	Sequence 104, App	908	27	29.3	252	7	US-11-054-515-1169	Sequence 1169, Ap
836	27	29.3	167	6	US-10-821-234-1589	Sequence 1589, Ap	909	27	29.3	252	7	US-11-054-515-1431	Sequence 1431, Ap
837	27	29.3	167	6	US-10-467-657-5908	Sequence 5908, Ap	910	27	29.3	253	6	US-10-821-234-1177	Sequence 1177, Ap
838	27	29.3	168	7	US-11-044-111-27	Sequence 27, Appl	911	27	29.3	253	6	US-10-467-657-8346	Sequence 8346, Ap
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840	27	29.3	172	7	US-11-024-959-306	Sequence 306, App	913	27	29.3	254	7	US-11-054-515-1295	Sequence 1295, Ap
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842	27	29.3	172	7	US-11-024-959-323	Sequence 323, App	915	27	29.3	254	7	US-11-054-515-1739	Sequence 1739, App
843	27	29.3	179	6	US-10-923-022-2	Sequence 2, Appli	916	27	29.3	255	7	US-11-156-084-161	Sequence 161, App
844	27	29.3	182	7	US-11-052-554A-5	Sequence 5, Appli	917	27	29.3	256	7	US-11-054-515-1183	Sequence 1183, Ap
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848	27	29.3	188	6	US-10-923-022-8	Sequence 8, Appli	921	27	29.3	261	7	US-11-124-368A-328	Sequence 328, App
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853	27	29.3	195	7	US-11-055-822-782	Sequence 782, App	926	27	29.3	273	7	US-11-152-366-50	Sequence 50, Appl
854	27	29.3	198	6	US-10-923-022-3	Sequence 3, Appli	927	27	29.3	281	6	US-10-834-397-178	Sequence 178, App
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856	27	29.3	199	6	US-10-995-561-902	Sequence 902, App	929	27	29.3	282	6	US-10-055-877-127	Sequence 127, App
857	27	29.3	199	6	US-10-923-022-5	Sequence 5, Appli	930	27	29.3	282	7	US-11-087-177-9	Sequence 9, Appli
858	27	29.3	200	6	US-10-923-022-10	Sequence 10, Appl	931	27	29.3	284	6	US-10-467-657-214	Sequence 214, App
859	27	29.3	206	6	US-10-798-579A-20	Sequence 20, Appl	932	27	29.3	284	6	US-10-467-657-3718	Sequence 3718, Ap
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861	27	29.3	212	6	US-10-821-234-890	Sequence 890, App	934	27	29.3	294	6	US-10-055-877-128	Sequence 128, App
862	27	29.3	212	6	US-10-714-887-368	Sequence 368, App	935	27	29.3	300	7	US-11-006-119-31	Sequence 31, Appl
863	27	29.3	216	6	US-10-793-626-4	Sequence 4, Appli	936	27	29.3	300	7	US-11-152-569-17	Sequence 17, Appl
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866	27	29.3	226	7	US-11-024-959-501	Sequence 501, App	939	27	29.3	305	6	US-10-055-877-126	Sequence 126, App
867	27	29.3	231	6	US-10-467-657-7948	Sequence 7948, Ap	940	27	29.3	305	6	US-10-055-877-264	Sequence 264, App
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870	27	29.3	236	6	US-10-714-887-180	Sequence 180, App	943	27	29.3	306	6	US-10-798-579A-26	Sequence 26, Appl
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872	27	29.3	238	6	US-10-467-657-6248	Sequence 6248, Ap	945	27	29.3	312	7	US-11-156-084-278	Sequence 278, App
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874	27	29.3	239	6	US-10-793-626-978	Sequence 978, App	947	27	29.3	313	7	US-11-000-463-427	Sequence 427, App
875	27	29.3	239	6	US-10-793-626-1696	Sequence 1696, Ap	948	27	29.3	319	6	US-10-793-626-2760	Sequence 2760, Ap
876	27	29.3	239	7	US-11-054-515-1922	Sequence 1922, Ap	949	27	29.3	320	6	US-10-453-372-854	Sequence 854, App
877	27	29.3	239	7	US-11-054-515-2018	Sequence 2018, Ap	950	27	29.3	327	7	US-11-129-143-89	Sequence 89, Appl
878	27	29.3	239	7	US-11-054-515-2022	Sequence 2028, Ap	951	27	29.3	331	6	US-10-432-483-25	Sequence 25, Appl
879	27	29.3	239	7	US-11-054-515-2023	Sequence 2028, Ap	952	27	29.3	336	6	US-10-714-887-342	Sequence 342, App
880	27	29.3	239	7	US-11-054-515-2035	Sequence 2038, Ap	953	27	29.3	336	6	US-10-485-788A-496	Sequence 496, App
881	27	29.3	240	6	US-10-925-366A-219	Sequence 219, App	954	27	29.3	341	7	US-11-083-800-10	Sequence 10, Appl
882	27	29.3	240	7	US-11-054-515-1886	Sequence 1886, Ap	955	27	29.3	346	7	US-11-000-365-52	Sequence 52, Appl
883	27	29.3	240	7	US-11-054-515-1918	Sequence 1918, Ap	956	27	29.3	346	7	US-11-032-794-52	Sequence 52, Appl
884	27	29.3	240	7	US-11-054-515-2047	Sequence 2047, Ap	957	27	29.3	347	6	US-10-793-626-106	Sequence 106, App
885	27	29.3	240	7	US-11-054-515-2052	Sequence 2052, Ap	958	27	29.3	358	6	US-10-525-674-46	Sequence 46, Appl
886	27	29.3	240	7	US-11-054-515-2059	Sequence 2059, Ap	959	27	29.3	365	7	US-11-087-177-5	Sequence 5, Appli
887	27	29.3	240	7	US-11-054-515-2061	Sequence 2061, Ap	960	27	29.3	370	6	US-10-821-234-1021	Sequence 1021, Ap
888	27	29.3	241	7	US-11-067-425A-72	Sequence 72, Appl	961	27	29.3	371	7	US-11-137-671-16	Sequence 16, Appl
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893	27	29.3	246	7	US-10-714-887-370	Sequence 370, App	966	27	29.3	389	7	US-11-047-757-2	Sequence 2, Appli
894	27	29.3	246	7	US-11-054-515-1324	Sequence 1324, Ap	967	27	29.3	389	7	US-11-166-892-17	Sequence 17, Appl
895	27	29.3	246	7	US-10-793-626-1975	Sequence 1475, Ap	968	27	29.3	392	6	US-10-793-626-2874	Sequence 2874, Ap
896	27	29.3	247	6	US-11-054-515-1969	Sequence 1476, Ap	969	27	29.3	392	6	US-10-453-372-632	Sequence 632, App
897	27	29.3	247	7	US-11-054-515-996	Sequence 996, App	970	27	29.3	392	6	US-10-878-556A-160	Sequence 160, App
898	27	29.3	247	7	US-11-054-515-1923	Sequence 1923, Ap	971	27	29.3	392	6	US-10-453-372-634	Sequence 634, App
899	27	29.3	248	7	US-11-054-515-921	Sequence 921, App	972	27	29.3	392	6	US-10-453-372-634	Sequence 634, App
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901	27	29.3	249	6	US-10-821-234-1125	Sequence 1125, Ap	974	27	29.3	396	6	US-10-453-372-620	Sequence 620, App

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975 27 29.3 401 7 US-11-000-365-50
976 27 29.3 401 7 US-11-032-794-50
977 27 29.3 408 6 US-10-821-234-1100
978 27 29.3 408 6 US-10-763-712A-67
979 27 29.3 417 6 US-10-821-234-1639
980 27 29.3 417 6 US-10-878-556A-52
981 27 29.3 422 6 US-10-336-263A-4
982 27 29.3 425 6 US-10-821-234-990
983 27 29.3 431 7 US-11-092-140-6
984 27 29.3 432 6 US-10-517-939-178
985 27 29.3 433 7 US-11-196-475-180
986 27 29.3 435 6 US-10-793-626-3186
987 27 29.3 439 7 US-11-112-882-18
988 27 29.3 442 6 US-10-453-372-618
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998 27 29.3 442 7 US-11-055-822-402
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ALIGNMENTS

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RESULT 1
US-11-175-690-321
; Sequence 321, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 321
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-321

Query Match 100.0%; Score 92; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. NO. 3.9e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLG 17
Db 10 CFGRKMDRISSSSLG 26

RESULT 2
US-11-175-690-322
; Sequence 322, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 322
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-322

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Best Local Similarity 100.0%; Pred. NO. 4.1e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLG 17
Db 10 CFGRKMDRISSSSLG 26

RESULT 3
US-11-175-690-371
; Sequence 371, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 371
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; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-371

Query Match 100.0%; Score 92; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.1e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 CFGRKMDRISSSSGLGC 26

RESULT 4
US-11-175-690-323
; Sequence 323, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 323
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-323

Query Match 100.0%; Score 92; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 CFGRKMDRISSSSGLGC 26

RESULT 5
US-11-175-690-369
; Sequence 369, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11

; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 369
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-369

Query Match 100.0%; Score 92; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
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Db 10 CFGRKMDRISSSSGLGC 26

RESULT 6
US-11-175-690-314
; Sequence 314, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 314
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-314

Query Match 100.0%; Score 92; DB 7; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.4e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 7
US-11-175-690-315
; Sequence 315, Application US/11175690

Publication No. US20060014254A1
GENERAL INFORMATION:
APPLICANT: Haseltine et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF605
CURRENT APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: PCT/US04/001369
PRIOR FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 60/441,305
PRIOR FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/453,201
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: US 60/467,222
PRIOR FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: US 60/472,816
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/476,267
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/505,172
PRIOR FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US 60/506,746
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 568
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 315
LENGTH: 29
TYPE: PRT
ORGANISM: Homo sapiens
US-11-175-690-315

Query Match 100.0%; Score 92; DB 7; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.4e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
|||||
DB 10 CFGRKMDRISSSSGLGC 26

RESULT 8
US-10-510-880-4
Sequence 4, Application US/10510880
Publication No. US20050244902A1
GENERAL INFORMATION:
APPLICANT: Rehfeld, Jens F.
APPLICANT: Goetze, Jens Peter
TITLE OF INVENTION: Methods for determining levels of human
TITLE OF INVENTION: B-type natriuretic peptide precursors
FILE REFERENCE: 27122000200
CURRENT APPLICATION NUMBER: US/10/510,880
CURRENT FILING DATE: 2004-10-08
PRIOR APPLICATION NUMBER: PCT/DK03/00250
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: PS1692
PRIOR FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 32
TYPE: PRT
ORGANISM: Homo sapiens
US-10-510-880-4

Query Match 100.0%; Score 92; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
|||||
DB 10 CFGRKMDRISSSSGLGC 26

RESULT 9
US-10-977-334-3
Sequence 3, Application US/10977334
Publication No. US20050244904A1
GENERAL INFORMATION:
APPLICANT: NG, LEONG
TITLE OF INVENTION: DIAGNOSTICS BASED ON SIGNAL PEPTIDE DETECTION
FILE REFERENCE: ISA-016.01
CURRENT APPLICATION NUMBER: US/10/977,334
CURRENT FILING DATE: 2004-10-29
PRIOR APPLICATION NUMBER: 60/542,647
PRIOR FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: GB 0325279.8
PRIOR FILING DATE: 2003-10-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 3
LENGTH: 32
TYPE: PRT
ORGANISM: Homo sapiens
US-10-977-334-3

Query Match 100.0%; Score 92; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
|||||
DB 10 CFGRKMDRISSSSGLGC 26

RESULT 10
US-11-043-590-17
Sequence 17, Application US/11043590
Publication No. US20050277156A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use therefor
FILE REFERENCE: 1847.1011
CURRENT APPLICATION NUMBER: US/11/043,590
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 17
LENGTH: 32
TYPE: PRT
ORGANISM: Homo sapiens
US-11-043-590-17

Query Match 100.0%; Score 92; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
|||||
DB 10 CFGRKMDRISSSSGLGC 26

RESULT 11
US-11-175-690-288
Sequence 288, Application US/11175690
Publication No. US20060014254A1
GENERAL INFORMATION:
APPLICANT: Haseltine et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF605
CURRENT APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: PCT/US04/001369
PRIOR FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 60/441,305
PRIOR FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/453,201

```

; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 288
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-288

```

Query Match 100.0%; Score 92; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 17; Conservative 0; Mismatches 0; Indels

Qy 1 CFGRKMDRISSSGLGC 17
Db 10 CFGRKMDRISSSGLGC 26

```

RESULT 12
US-11-175-690-298
; Sequence 298, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF6005
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/457,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 298
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-298

```

```
Query Match      100.0%; Score 92; DB 7; Length 32;
Best Local Similarity 100.0%; Pred.No. 4.9e-10;
Matches 17; Conservative 0; Mismatches 0; Indels
```

Qy 1 CFGRKMDRISSSSLGC 17
Db 10 CFGRKMDRISSSSLGC 26

RESULT 13
US-11-175-690-304

```

; Sequence 304, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
;
; APPLICANT: Haseltine et al.
;
; TITLE OF INVENTION: Albumin Fusion Proteins
;
; FILE REFERENCE: PG605
;
; CURRENT APPLICATION NUMBER: US/11/175,690
;
; CURRENT FILING DATE: 2005-07-07
;
; PRIOR APPLICATION NUMBER: PCT/US04/001369
;
; PRIOR FILING DATE: 2004-01-20
;
; PRIOR APPLICATION NUMBER: US 60/441,305
;
; PRIOR FILING DATE: 2003-01-22
;
; PRIOR APPLICATION NUMBER: US 60/453,201
;
; PRIOR FILING DATE: 2003-03-11
;
; PRIOR APPLICATION NUMBER: US 60/467,222
;
; PRIOR FILING DATE: 2003-05-02
;
; PRIOR APPLICATION NUMBER: US 60/472,816
;
; PRIOR FILING DATE: 2003-05-23
;
; PRIOR APPLICATION NUMBER: US 60/476,267
;
; PRIOR FILING DATE: 2003-06-06
;
; PRIOR APPLICATION NUMBER: US 60/505,172
;
; PRIOR FILING DATE: 2003-09-24
;
; PRIOR APPLICATION NUMBER: US 60/506,746
;
; PRIOR FILING DATE: 2003-09-30
;
; NUMBER OF SEQ ID NOS: 568
;
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 304
;
; LENGTH: 32
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
; US-11-175-690-304

```

Query Match 100.0%; Score 92; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 17; Conservative 0; Mismatches 0; Indels

Qy 1 CFGRKMDRISSSSGLGC 17
|||
Db 10 CFGRKMDRISSSSGLGC 26

```

RESULT 14
US-11-175-690-317
; Sequence 317, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFG05
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 317
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-11-175-690-317

Query Match 100.0%; Score 92; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | | | |
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 15

US-11-175-690-318
; Sequence 318, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 318
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-175-690-318

Query Match 100.0%; Score 92; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | | | |
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 16

US-11-175-690-370
; Sequence 370, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816

; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 370
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-370

Query Match 100.0%; Score 92; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | | | |
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 17

US-11-043-590-15
; Sequence 15, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use therefor
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 15
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-590-15

Query Match 100.0%; Score 92; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CFGRKMDRISSSSGLGC 36

RESULT 18

US-11-175-690-368
; Sequence 368, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172

; PRIOR FILING DATE: 2003-09-24
 ; PRIOR APPLICATION NUMBER: US 60/506,746
 ; PRIOR FILING DATE: 2003-09-30
 ; NUMBER OF SEQ ID NOS: 568
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 368
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-175-690-368

Query Match 100.0%; Score 92; DB 7; Length 52;
 Best Local Similarity 100.0%; Pred. No. 8.1e-10;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 Db 10 CFGRKMDRISSSSGLGC 26

RESULT 19
 US-11-043-590-16
 ; Sequence 16, Application US/11043590
 ; Publication No. US20050271156A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen Ltd
 ; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use there
 ; FILE REFERENCE: 1847.1011
 ; CURRENT APPLICATION NUMBER: US/11/043,590
 ; CURRENT FILING DATE: 2005-01-27
 ; NUMBER OF SEQ ID NOS: 47
 ; SEQ ID NO 16
 ; LENGTH: 60
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-043-590-16

Query Match 100.0%; Score 92; DB 7; Length 60;
 Best Local Similarity 100.0%; Pred. No. 9.4e-10;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 Db 10 CFGRKMDRISSSSGLGC 26

RESULT 20
 US-10-510-880-5
 ; Sequence 5, Application US/10510880
 ; Publication No. US20050244902A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rehfeld, Jens F.
 ; APPLICANT: Goetze, Jens Peter
 ; APPLICANT: Righesopitalet
 ; TITLE OF INVENTION: Methods for determining levels of human
 ; FILE REFERENCE: 271212000200
 ; CURRENT APPLICATION NUMBER: US/10/510,880
 ; CURRENT FILING DATE: 2004-10-08
 ; PRIOR APPLICATION NUMBER: PCT/DK03/00250
 ; PRIOR FILING DATE: 2003-04-11
 ; PRIOR APPLICATION NUMBER: PSI692
 ; PRIOR FILING DATE: 2002-04-11
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-510-880-5

Query Match 100.0%; Score 92; DB 6; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.7e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CFGRKMDRISSSSGLGC 17
 Db 86 CFGRKMDRISSSSGLGC 102

RESULT 21
 US-10-875-800-1
 ; Sequence 1, Application US/10875800
 ; Publication No. US20050255484A1
 ; GENERAL INFORMATION:
 ; APPLICANT: VALKIES, GUNARS
 ; APPLICANT: DAHLEN, JEFF
 ; APPLICANT: KIRCHICK, HOWARD
 ; APPLICANT: BUECHLER, KEN
 ; TITLE OF INVENTION: DIAGNOSTIC MARKERS OF STROKE AND CEREBRAL INJURY AND
 ; FILE REFERENCE: 071949-5408
 ; CURRENT APPLICATION NUMBER: US/10/875,800
 ; CURRENT FILING DATE: 2004-06-23
 ; PRIOR APPLICATION NUMBER: US/10/714,078
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 10/371,149
 ; PRIOR FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 10/225,082
 ; PRIOR FILING DATE: 2002-08-20
 ; PRIOR APPLICATION NUMBER: PCT/US02/26604
 ; PRIOR FILING DATE: 2002-08-20
 ; PRIOR APPLICATION NUMBER: 60/313,775
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: 60/334,964
 ; PRIOR FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: 60/346,485
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Patent in Ver. 3.2
 ; SEQ ID NO 1
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-875-800-1

Query Match 100.0%; Score 92; DB 6; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 Db 86 CFGRKMDRISSSSGLGC 102

RESULT 22
 US-10-299-977-1
 ; Sequence 1, Application US/10299977
 ; Publication No. US20050287613A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jackowski, George
 ; APPLICANT: Kupchak, Peter
 ; APPLICANT: Stanton, Eric
 ; APPLICANT: Davey, Michelle
 ; TITLE OF INVENTION: Polyclonal-Polyclonal ELISA Assay For Detecting N-Terminus ProBN
 ; FILE REFERENCE: 2132.127
 ; CURRENT APPLICATION NUMBER: US/10/299,977
 ; CURRENT FILING DATE: 2002-11-18
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-299-977-1

Query Match 100.0%; Score 92; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | | |
Db 86 CFGRKMDRISSSSGLGC 102

RESULT 23
US-10-510-880-1
; Sequence 1, Application US/10510880
; Publication No. US20050244902A1
; GENERAL INFORMATION:
; APPLICANT: Rehfeld, Jens F.
; APPLICANT: Goetze, Jens Peter
; APPLICANT: Righospitalet
; TITLE OF INVENTION: Methods for determining levels of human
; FILE OF INVENTION: B-type natriuretic peptide precursors
; FILE REFERENCE: 271212000200
; CURRENT APPLICATION NUMBER: US/10/510,880
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: PCT/DK03/00250
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PS1692
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-880-1

Query Match 100.0%; Score 92; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | | |
Db 112 CFGRKMDRISSSSGLGC 128

RESULT 24
US-10-875-800-2
; Sequence 2, Application US/10875800
; Publication No. US20050255484A1
; GENERAL INFORMATION:
; APPLICANT: VALKIRS, GUNARS
; APPLICANT: DAHLEN, JEFF
; APPLICANT: KIRCHICK, HOWARD
; APPLICANT: BUECHLER, KEN
; TITLE OF INVENTION: DIAGNOSTIC MARKERS OF STROKE AND CEREBRAL INJURY AND
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 071949-5408
; CURRENT APPLICATION NUMBER: US/10/875,800
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/10/714,078
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 10/371,149
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/225,082
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT/US02/26604
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/313,775
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/334,964
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/346,485
; PRIOR FILING DATE: 2002-01-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-875-800-2

Query Match 100.0%; Score 92; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | | |
Db 112 CFGRKMDRISSSSGLGC 128

RESULT 25
US-11-043-590-12
; Sequence 12, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use there
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-590-12

Query Match 100.0%; Score 92; DB 7; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | | |
Db 112 CFGRKMDRISSSSGLGC 128

RESULT 26
US-11-043-590-13
; Sequence 13, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use there
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 13
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-590-13

Query Match 100.0%; Score 92; DB 7; Length 162;
Best Local Similarity 100.0%; Pred. No. 2.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | | |
Db 112 CFGRKMDRISSSSGLGC 128

RESULT 27
US-11-175-690-234
; Sequence 234, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.

; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 234
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-234

Query Match 100.0%; Score 92; DB 7; Length 630;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 29 CFGRKMDRISSSSGLGC 45

RESULT 28
US-11-175-690-235
; Sequence 235, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 235
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-235

Query Match 100.0%; Score 92; DB 7; Length 631;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
Db 29 CFGRKMDRISSSSGLGC 45

RESULT 29
US-11-175-690-236
; Sequence 236, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 236
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-236

Query Match 100.0%; Score 92; DB 7; Length 632;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 29 CFGRKMDRISSSSGLGC 45

RESULT 30
US-11-175-690-228
; Sequence 228, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172

```
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 228
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-228
```

```
Query Match 100.0%; Score 92; DB 7; Length 633;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CFGRKMDRISSSSGLGC 17
      |||||||
Db 29 CFGRKMDRISSSSGLGC 45
```

```
RESULT 31
US-11-175-690-211
; Sequence 211, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 211
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-211
```

```
Query Match 100.0%; Score 92; DB 7; Length 641;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CFGRKMDRISSSSGLGC 17
      |||||||
Db 34 CFGRKMDRISSSSGLGC 50
```

```
RESULT 32
US-11-175-690-230
; Sequence 230, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
```

```
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 230
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-230
```

```
Query Match 100.0%; Score 92; DB 7; Length 641;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CFGRKMDRISSSSGLGC 17
      |||||||
Db 34 CFGRKMDRISSSSGLGC 50
```

```
RESULT 33
US-11-175-690-281
; Sequence 281, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 281
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-281
```

```
Query Match 100.0%; Score 92; DB 7; Length 661;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CFGRKMDRISSSSGLGC 17
      |||||||
```

Db 34 CFGRKMDRISSSSGLGC 50

RESULT 34

US-11-175-690-284

Sequence 284, Application US/11175690

Publication No. US20060014254A1

GENERAL INFORMATION:

APPLICANT: Haseltine et al.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF605

CURRENT APPLICATION NUMBER: US/11/175,690

CURRENT FILING DATE: 2005-07-07

PRIOR APPLICATION NUMBER: PCT/US04/001369

PRIOR FILING DATE: 2004-01-20

PRIOR APPLICATION NUMBER: US 60/441,305

PRIOR FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: US 60/453,201

PRIOR FILING DATE: 2003-03-11

PRIOR APPLICATION NUMBER: US 60/467,222

PRIOR FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: US 60/472,816

PRIOR FILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: US 60/476,267

PRIOR FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: US 60/505,172

PRIOR FILING DATE: 2003-09-24

PRIOR APPLICATION NUMBER: US 60/506,746

PRIOR FILING DATE: 2003-09-30

NUMBER OF SEQ ID NOS: 568

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 284

LENGTH: 663

TYPE: PRT

ORGANISM: Homo sapiens

US-11-175-690-284

Query Match 100.0%; Score 92; DB 7; Length 663;

Best Local Similarity 100.0%; Pred. No. 1.2e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17

Db 34 CFGRKMDRISSSSGLGC 50

RESULT 35

US-11-175-690-282

Sequence 282, Application US/11175690

Publication No. US20060014254A1

GENERAL INFORMATION:

APPLICANT: Haseltine et al.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF605

CURRENT APPLICATION NUMBER: US/11/175,690

CURRENT FILING DATE: 2005-07-07

PRIOR APPLICATION NUMBER: PCT/US04/001369

PRIOR FILING DATE: 2004-01-20

PRIOR APPLICATION NUMBER: US 60/441,305

PRIOR FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: US 60/453,201

PRIOR FILING DATE: 2003-03-11

PRIOR APPLICATION NUMBER: US 60/467,222

PRIOR FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: US 60/472,816

PRIOR FILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: US 60/476,267

PRIOR FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: US 60/505,172

PRIOR FILING DATE: 2003-09-24

PRIOR APPLICATION NUMBER: US 60/506,746

PRIOR FILING DATE: 2003-09-30

NUMBER OF SEQ ID NOS: 568

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 282

LENGTH: 665

TYPE: PRT

ORGANISM: Homo sapiens

US-11-175-690-282

Query Match 100.0%; Score 92; DB 7; Length 665;

Best Local Similarity 100.0%; Pred. No. 1.2e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17

Db 34 CFGRKMDRISSSSGLGC 50

RESULT 36

US-11-175-690-227

Sequence 227, Application US/11175690

Publication No. US20060014254A1

GENERAL INFORMATION:

APPLICANT: Haseltine et al.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF605

CURRENT APPLICATION NUMBER: US/11/175,690

CURRENT FILING DATE: 2005-07-07

PRIOR APPLICATION NUMBER: PCT/US04/001369

PRIOR FILING DATE: 2004-01-20

PRIOR APPLICATION NUMBER: US 60/441,305

PRIOR FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: US 60/453,201

PRIOR FILING DATE: 2003-03-11

PRIOR APPLICATION NUMBER: US 60/467,222

PRIOR FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: US 60/472,816

PRIOR FILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: US 60/476,267

PRIOR FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: US 60/505,172

PRIOR FILING DATE: 2003-09-24

PRIOR APPLICATION NUMBER: US 60/506,746

PRIOR FILING DATE: 2003-09-30

NUMBER OF SEQ ID NOS: 568

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 227

LENGTH: 667

TYPE: PRT

ORGANISM: Homo sapiens

US-11-175-690-227

Query Match 100.0%; Score 92; DB 7; Length 667;

Best Local Similarity 100.0%; Pred. No. 1.2e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17

Db 34 CFGRKMDRISSSSGLGC 50

RESULT 37

US-11-175-690-283

Sequence 283, Application US/11175690

Publication No. US20060014254A1

GENERAL INFORMATION:

APPLICANT: Haseltine et al.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF605

CURRENT APPLICATION NUMBER: US/11/175,690

CURRENT FILING DATE: 2005-07-07

PRIOR APPLICATION NUMBER: PCT/US04/001369

PRIOR FILING DATE: 2004-01-20

PRIOR APPLICATION NUMBER: US 60/441,305

PRIOR FILING DATE: 2003-01-22

; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 283
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-283

Query Match 100.0%; Score 92; DB 7; Length 670;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
||| ||||| ||||| |||||
DB 31 CFGRKMDRISSSSGLGC 47

RESULT 38
US-11-175-690-201
; Sequence 201, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 201
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-201

Query Match 100.0%; Score 92; DB 7; Length 673;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
||| ||||| ||||| |||||
DB 34 CFGRKMDRISSSSGLGC 50

RESULT 39

US-11-175-690-217
; Sequence 217, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 217
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-217

Query Match 100.0%; Score 92; DB 7; Length 673;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
||| ||||| ||||| |||||
DB 34 CFGRKMDRISSSSGLGC 50

RESULT 40
US-11-175-690-231
; Sequence 231, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 231
; LENGTH: 673
; TYPE: PRT

```

; ORGANISM: Homo sapiens
US-11-175-690-231

Query Match      100.0%; Score 92; DB 7; Length 673;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSGLGC 17
DB 34 CFCGRKMDRISSSSGLGC 50

RESULT 41
US-10-510-880-2
; Sequence 2, Application US/10510880
; Publication No. US20050244902A1
; GENERAL INFORMATION:
; APPLICANT: Rehfeld, Jens F.
; APPLICANT: Goetze, Jens Peter
; APPLICANT: Righespositalet
; TITLE OF INVENTION: Methods for determining levels of human
; FILE REFERENCE: 271212000200
; CURRENT APPLICATION NUMBER: US/10/510,880
; PRIOR FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: PCT/DK03/00250
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PS1692
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-510-880-2

Query Match      82.6%; Score 76; DB 6; Length 131;
Best Local Similarity 76.5%; Pred. No. 1.4e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSGLGC 17
DB 109 CFCGRKMDRISSSSGLGC 125

RESULT 42
US-10-977-334-5
; Sequence 5, Application US/10977334
; Publication No. US20050244904A1
; GENERAL INFORMATION:
; APPLICANT: NG, LEONG
; TITLE OF INVENTION: DIAGNOSTICS BASED ON SIGNAL PEPTIDE DETECTION
; FILE REFERENCE: ISA-016.01
; CURRENT APPLICATION NUMBER: US/10/977,334
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/542,647
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: GB 0325279.8
; PRIOR FILING DATE: 2003-10-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-334-5

Query Match      79.3%; Score 73; DB 6; Length 126;
Best Local Similarity 76.5%; Pred. No. 4.5e-06;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSGLGC 17

```

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DB 110 CFCGLKLDRISSSSGLGC 126

RESULT 43
US-11-112-277-16
; Sequence 16, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; TITLE OF INVENTION: CONJUGATES
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANP Analogue
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa is Ser linked to AEEA-MPA
US-11-112-277-16

Query Match      77.2%; Score 71; DB 7; Length 28;
Best Local Similarity 70.6%; Pred. No. 2.1e-06;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFCGRKMDRISSSSGLGC 17
DB 7 CFCGRMDRIGAQSGLGC 23

RESULT 44
US-11-112-277-50
; Sequence 50, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; TITLE OF INVENTION: CONJUGATES
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANP Analogue
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa is Ser linked to MPA
US-11-112-277-50

Query Match      77.2%; Score 71; DB 7; Length 28;
Best Local Similarity 70.6%; Pred. No. 2.1e-06;

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Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   ||| : ||| : |||
Db 7 CFGRMDRIGAQSGLC 23

RESULT 45
US-11-112-277-51
; Sequence 51, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; TITLE OF INVENTION: CONJUGATES
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANP Analogue
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa is Ser linked to EEEP-MPA
US-11-112-277-51

Query Match 77.2%; Score 71; DB 7; Length 28;
Best Local Similarity 70.6%; Pred. No. 2.1e-06;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   ||| : ||| : |||
Db 7 CFGRMDRIGAQSGLC 23

RESULT 46
US-11-059-814-4
; Sequence 4, Application US/11059814
; Publication No. US20050272650A1
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Mohapatra, Shyam
; TITLE OF INVENTION: Materials and Methods for Treatment of Inflammatory and Cell
; TITLE OF INVENTION: Proliferation Disorders
; FILE REFERENCE: USF-215PTCZ
; CURRENT APPLICATION NUMBER: US/11/059,814
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/521,072
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-059-814-4

Query Match 77.2%; Score 71; DB 7; Length 28;
Best Local Similarity 70.6%; Pred. No. 2.1e-06;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   ||| : ||| : |||
Db 7 CFGRMDRIGAQSGLC 23

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   ||| : ||| : |||
Db 7 CFGRMDRIGAQSGLC 23

Db 7 CFGRMDRIGAQSGLC 23

RESULT 47
US-11-175-690-309
; Sequence 309, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 309
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-309

Query Match 77.2%; Score 71; DB 7; Length 28;
Best Local Similarity 70.6%; Pred. No. 2.1e-06;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   ||| : ||| : |||
Db 7 CFGRMDRIGAQSGLC 23

RESULT 48
US-11-059-814-7
; Sequence 7, Application US/11059814
; Publication No. US20050272650A1
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Mohapatra, Shyam
; TITLE OF INVENTION: Materials and Methods for Treatment of Inflammatory and Cell
; TITLE OF INVENTION: Proliferation Disorders
; FILE REFERENCE: USF-215PTCZ
; CURRENT APPLICATION NUMBER: US/11/059,814
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/521,072
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-059-814-7

Query Match 77.2%; Score 71; DB 7; Length 151;
Best Local Similarity 70.6%; Pred. No. 1.2e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   ||| : ||| : |||
Db 7 CFGRMDRIGAQSGLC 23
```


Db 130 CFGRMDRIGASGLGC 146
 ||| :|||| : |||||

RESULT 49
 US-10-977-334-4
 ; Sequence 4, Application US/10977334
 ; Publication No. US20050244904A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NG, LEONG
 ; TITLE OF INVENTION: DIAGNOSTICS BASED ON SIGNAL PEPTIDE DETECTION
 ; FILE REFERENCE: ISA-016.01
 ; CURRENT APPLICATION NUMBER: US/10/977,334
 ; CURRENT FILING DATE: 2004-10-29
 ; PRIOR APPLICATION NUMBER: 60/542,647
 ; PRIOR FILING DATE: 2004-02-06
 ; PRIOR APPLICATION NUMBER: GB 0325279.8
 ; PRIOR FILING DATE: 2003-10-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patentin Ver. 3.3
 ; SEQ ID NO 4
 ; LENGTH: 153
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-977-334-4

Query Match 77.2%; Score 71; DB 6; Length 153;
 Best Local Similarity 70.6%; Pred. No. 1.2e-05;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRMDRISSSSGLGC 17
 ||| :|||| : |||||
 Db 130 CFGRMDRIGASGLGC 146

RESULT 50
 US-11-175-690-222
 ; Sequence 222, Application US/11175690
 ; Publication No. US20060014254A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haseltine et al.
 ; TITLE OF INVENTION: Albumin Fusion Proteins
 ; FILE REFERENCE: PF605
 ; CURRENT APPLICATION NUMBER: US/11/175,690
 ; CURRENT FILING DATE: 2005-07-07
 ; PRIOR APPLICATION NUMBER: PCT/US04/001369
 ; PRIOR FILING DATE: 2004-01-20
 ; PRIOR APPLICATION NUMBER: US 60/441,305
 ; PRIOR FILING DATE: 2003-01-22
 ; PRIOR APPLICATION NUMBER: US 60/453,201
 ; PRIOR FILING DATE: 2003-03-11
 ; PRIOR APPLICATION NUMBER: US 60/467,222
 ; PRIOR FILING DATE: 2003-05-02
 ; PRIOR APPLICATION NUMBER: US 60/472,816
 ; PRIOR FILING DATE: 2003-05-23
 ; PRIOR APPLICATION NUMBER: US 60/476,267
 ; PRIOR FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: US 60/505,172
 ; PRIOR FILING DATE: 2003-09-24
 ; PRIOR APPLICATION NUMBER: US 60/506,746
 ; PRIOR FILING DATE: 2003-09-30
 ; NUMBER OF SEQ ID NOS: 568
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 222
 ; LENGTH: 637
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-175-690-222

Query Match 77.2%; Score 71; DB 7; Length 637;
 Best Local Similarity 70.6%; Pred. No. 5.5e-05;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRMDRISSSSGLGC 17
 ||| :|||| : |||||
 Db 31 CFGRMDRIGASGLGC 47
 Search completed: January 25, 2006, 18:50:06
 Job time : 10 secs

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OM protein - protein search, using sw model

Run on: January 25, 2006, 18:42:42 ; Search time 16 Seconds

(without alignments)
102.230 Million cell updates/sec

Title: US-10-737-290-172

Perfect score: 92
Sequence: 1 CPGKMDRISSSGLGC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR 80.*

1: piri.*

2: piri2.*

3: piri3.*

4: piri4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	134	1 AWHUB	natriuretic peptid
2	76	82.6	27	2 JC1081	brain natriuretic
3	76	82.6	103	2 A41403	aldosterone secret
4	76	82.6	105	2 B36736	brain natriuretic
5	76	82.6	131	2 A31676	brain natriuretic
6	76	82.6	131	2 A33873	brain natriuretic
7	74	80.4	38	2 S71381	lebetin 2 isoform
8	73	79.3	126	1 A36155	natriuretic peptid
9	73	79.3	126	1 AWHUC	natriuretic peptid
10	73	79.3	126	2 A55688	natriuretic peptid
11	73	79.3	126	2 S12988	brain natriuretic
12	73	79.3	140	1 S14320	alpha-atrial natri
13	72	78.3	22	2 JT0581	natriuretic peptid
14	72	78.3	22	2 A35418	brain natriuretic
15	72	78.3	27	2 A34431	atrial natriuretic
16	72	78.3	36	2 S15821	ventricular natriu
17	71	77.2	149	1 AWDG	atrial natriuretic
18	71	77.2	150	1 S13107	atrial natriuretic
19	71	77.2	151	1 AWHU	natriuretic peptid
20	71	77.2	152	1 AWHB	atrial natriuretic
21	71	77.2	153	2 S14873	atrial natriuretic
22	71	77.2	161	4 I55480	hypothetical natri
23	70	76.1	118	2 B54119	C-type natriuretic
24	70	76.1	135	1 A61244	natriuretic peptid
25	69	75.0	115	2 S15822	natriuretic peptid
26	68	73.9	22	2 A36399	C-type natriuretic
27	68	73.9	129	1 A54119	C-type natriuretic
28	67	72.8	152	1 AWHM	atrial natriuretic
29	67	72.8	152	1 AWR	atrial natriuretic

atrial natriuretic	153	72.8	67	30	AWRB
atrial natriuretic	30	71.7	66	31	S01657
atrial natriuretic	145	71.7	66	32	JQ0947
type-B natriuretic	121	70.7	65	33	A49144
brain natriuretic	121	70.7	65	34	I49548
atrial natriuretic	128	70.7	65	35	S14872
natriuretic peptid	38	68.5	63	36	A42974
brain natriuretic	121	68.5	63	37	A30162
acetyl-CoA:acetoac	496	47.8	44	38	AH3254
F12G12.17 protein	231	46.7	43	39	H86463
hypothetical prote	522	46.7	40	40	T24265
pyruvate synthase	273	45.7	42	41	F64593
chain of 2-oxogluc	273	45.7	42	42	H71919
serine/threonine-s	436	45.7	42	43	T51402
yahr protein - Esc	148	44.6	44	44	D64760
transcription regu	307	44.6	45	45	T41462
probable acyl-CoA	523	44.6	46	46	B95358
hypothetical prote	738	44.6	47	47	B87627
alpha-galactosidas	746	44.6	48	48	S74219
bacteriophage prot	757	44.6	49	49	AF1755
probable outer mem	797	44.6	50	50	H83190
hypothetical prote	970	44.0	51	51	C84488
hypothetical prote	163	43.5	52	52	T48772
probable brain rya	683	43.5	53	53	I47214
serine/threonine-s	707	43.5	54	54	T38254
drebrin A - rat	2703	43.5	55	55	S60588
hemagglutinin/hemo	4859	43.5	56	56	H81193
ryanodine receptor	2	43.5	57	57	S74173
ryanodine receptor	2	43.5	58	58	S66572
ryanodine receptor	2	43.5	59	59	S27272
hemolysin A precu	1577	42.9	60	60	A35140
hypothetical prote	107	42.4	61	61	B71069
hypothetical prote	126	42.4	62	62	T21199
exodeoxyribonucle	267	42.4	63	63	C97690
exodeoxyribonucle	267	42.4	64	64	AH2915
hypothetical prote	327	42.4	65	65	S55628
hypothetical prote	338	42.4	66	66	G96685
hypothetical prote	444	42.4	67	67	T24204
probable PPE prote	590	42.4	68	68	E70946
probable oxidoredu	747	42.4	69	69	B95363
translation elonga	813	42.4	70	70	T40622
agglutinin-like pr	1260	42.4	71	71	S60896
filamentous hemagg	3591	42.4	72	72	S21010
RNA-directed DNA p	1051	41.8	73	73	B27672
hypothetical prote	1330	41.8	74	74	C84716
hypothetical prote	246	41.3	75	75	T08584
probable phosphate	319	41.3	76	76	G81409
other proteins homo	319	41.3	77	77	AD1108
conserved hypotet	349	41.3	78	78	AE1469
lectin-like protei	353	41.3	79	79	E95858
alpha-complex prot	356	41.3	80	80	T45949
choline transport	563	41.3	81	81	S58529
probable translati	683	41.3	82	82	S11175
hypothetical prote	803	41.3	83	83	C71322
translation elonga	819	41.3	84	84	S45916
two component sens	893	41.3	85	85	A43748
two-component sens	900	41.3	86	86	AG3022
calmodulin-binding	1022	41.3	87	87	C98262
pol protein - silk	1067	41.3	88	88	T51257
phytochrome A - Po	1125	41.3	89	89	T18196
P Type Copper ATPa	904	41.3	90	90	T09835
F17F16.1 protein -	2142	40.8	91	91	T40072
hypothetical prote	77	40.2	92	92	D86303
hypothetical prote	127	40.2	93	93	H83974
hypothetical prote	138	40.2	94	94	G84720
hypothetical prote	164	40.2	95	95	D72727
hypothetical prote	187	40.2	96	96	B82773
hypothetical prote	213	40.2	97	97	S69569
hypothetical prote	260	40.2	98	98	G86195
probable permeal	260	40.2	99	99	E98219
hypothetical prote	267	40.2	100	100	E98219
corticotropin / li	281	40.2	101	101	AE3067
2-oxoglutarate syn	281	40.2	102	102	CTHUP
					A81400

103	37	40.2	286	2	A69005	2-oxoglutarate syn	176	36	39.1	475	2	S48132	metalloproteinase
104	37	40.2	303	2	F82549	hypothetical prote	177	36	39.1	478	1	C42790	cystathionine beta
105	37	40.2	307	2	JC5036	hypothetical prote	178	36	39.1	488	2	T10258	gag polyprotein ho
106	37	40.2	317	2	C70863	hypothetical prote	179	36	39.1	490	2	S49792	probable membrane
107	37	40.2	332	2	T26436	hypothetical prote	180	36	39.1	496	2	JC5261	salt-tolerant prot
108	37	40.2	349	2	T23114	hypothetical prote	181	36	39.1	504	2	T21377	hypothetical prote
109	37	40.2	361	2	A86386	probable DNA-bind	182	36	39.1	524	2	S66467	alkaline phosphat
110	37	40.2	373	2	A84699	hypothetical prote	183	36	39.1	551	2	A12964	hypothetical prote
111	37	40.2	376	2	A75381	peptide ABC transp	184	36	39.1	561	1	A42790	cystathionine beta
112	37	40.2	468	2	T40223	HMG-box containin	185	36	39.1	564	2	T42695	hypothetical prote
113	37	40.2	468	2	A41518	transcription fact	186	36	39.1	579	2	T50228	conserved hypothet
114	37	40.2	508	2	G81205	sodium/proline sym	187	36	39.1	593	1	JT0742	tartarone-semiald
115	37	40.2	589	2	D81905	probable sulfite r	188	36	39.1	593	2	AH0566	glyoxylate carboli
116	37	40.2	594	2	D96015	probable tartronat	189	36	39.1	593	2	C85550	glyoxylate carboli
117	37	40.2	624	2	T41341	probable serine-th	190	36	39.1	601	2	G96558	probable protein k
118	37	40.2	776	2	T02584	probable protein k	191	36	39.1	601	2	G96558	hypothetical prote
119	37	40.2	783	2	E96652	protein F23N19.11	192	36	39.1	607	2	S53387	hypothetical prote
120	37	40.2	787	2	S35701	translation elonga	193	36	39.1	617	2	T23014	hypothetical prote
121	37	40.2	818	2	S62790	mismatch DNA recog	194	36	39.1	619	2	T48557	hypothetical prote
122	37	40.2	970	2	JQ0302	hypothetical 112K	195	36	39.1	622	2	T27155	hypothetical prote
123	37	40.2	1075	2	A57377	transcription fact	196	36	39.1	690	2	D98318	ABC protein AGR_L
124	37	40.2	1247	2	T231331	nitric-oxide synth	197	36	39.1	691	2	A71520	hypothetical prote
125	37	40.2	1258	2	T29041	hypothetical prote	198	36	39.1	694	2	A83126	probable TonB-depe
126	37	40.2	1261	2	T13165	mutator 2 - fruit	199	36	39.1	752	2	AC3624	acriflavin resista
127	37	40.2	2143	2	G96595	hypothetical prote	200	36	39.1	755	1	QOAG4T	tryptophan 2-mono
128	37	40.2	2510	2	T28160	hypothetical prote	201	36	39.1	763	2	S23457	polysulfide reduct
129	37	40.2	5032	1	A35041	ryanodine receptor	202	36	39.1	770	2	G02228	DOC-2 - human
130	37	40.2	5035	1	I46646	ryanodine receptor	203	36	39.1	798	2	C96658	probable RNA helic
131	37	40.2	5037	1	A54161	ryanodine-binding	204	36	39.1	818	2	T31464	hypothetical prote
132	37	40.2	5037	2	B35041	ryanodine receptor	205	36	39.1	822	2	T33163	related to tol pro
133	36.5	39.7	140	2	S20914	lysosome (EC 3.2.1	206	36	39.1	824	2	T51057	probable RNA helic
134	36.5	39.7	140	2	S41573	lysosome (EC 3.2.1	207	36	39.1	845	2	E84488	related to tol pro
135	36.5	39.7	424	2	E86367	protein F26F24.22	208	36	39.1	860	2	JC5702	Erbb kinase activa
136	36.5	39.7	729	2	AH2857	anthranilate synth	209	36	39.1	868	2	T26775	Erbb kinase activa
137	36.5	39.7	729	2	F97634	anthranilate synth	210	36	39.1	902	2	T26775	hypothetical prote
138	36	39.1	57	2	C97283	ribosomal protein	211	36	39.1	956	2	S30834	hypothetical prote
139	36	39.1	107	2	S52508	probable membrane	212	36	39.1	964	2	T05382	hypothetical prote
140	36	39.1	118	2	T08723	hypothetical prote	213	36	39.1	1392	1	YGBVAD	L-aminoadipate-sem
141	36	39.1	133	2	JH0270	chondromodulin II	214	36	39.1	1507	2	A40228	neurexin I-alpha p
142	36	39.1	164	2	E69874	conserved hypothet	215	36	39.1	1530	2	I45944	neurexin I-alpha -
143	36	39.1	183	2	C83913	hypothetical prote	216	36	39.1	1753	2	T00350	hypothetical prote
144	36	39.1	198	2	T28814	hypothetical prote	217	36	39.1	1958	2	T39808	hypothetical prote
145	36	39.1	201	2	F72390	hypothetical prote	218	36	39.1	2023	2	T13154	polycarb protein e
146	36	39.1	243	1	VH0UPT	nucleocapsid prote	219	36	39.1	2195	2	T34264	hypothetical prote
147	36	39.1	262	2	AE2607	conserved hypothet	220	36	39.1	4767	2	T31345	hypothetical prote
148	36	39.1	263	2	H83042	hypothetical prote	221	36	39.1	4868	2	B54161	ryanodine-binding
149	36	39.1	265	2	C69978	glutamate racemase	222	35.5	38.6	91	4	SL4968	hypothetical NADH
150	36	39.1	266	2	T05471	hypothetical prote	223	35.5	38.6	146	2	E84489	40S ribosomal prot
151	36	39.1	272	2	D97389	hypothetical prote	224	35.5	38.6	196	2	D96546	hypothetical prote
152	36	39.1	288	2	E83946	pyruvate synthase	225	35.5	38.6	297	2	B83681	ABC transporter (p
153	36	39.1	293	2	AE0977	probable sugar kin	226	35.5	38.6	485	2	JC4363	glucagon receptor
154	36	39.1	307	2	AG2017	glycerol-3-phospha	227	35.5	38.6	485	2	QJ1957	glucagon receptor
155	36	39.1	309	2	E84672	hypothetical prote	228	35.5	38.6	500	2	T04737	cytochrome P450 ho
156	36	39.1	320	2	PN0090	aspergillopepsin I	229	35.5	38.6	500	2	T52175	cytochrome P450 mo
157	36	39.1	321	2	D96035	probable transposa	230	35.5	38.6	849	1	UYPVAD	noncapsid protein
158	36	39.1	321	2	E96025	probable transposa	231	35.5	38.6	1055	2	T10432	DNA-directed RNA p
159	36	39.1	329	2	A84529	hypothetical prote	232	35.5	38.6	1884	2	JC4975	plexin 2 precursor
160	36	39.1	333	2	H85551	hypothetical prote	233	35.5	38.6	2437	2	S42612	transmembrane prot
161	36	39.1	333	2	E90701	hypothetical prote	234	35	38.0	70	2	C83620	hypothetical prote
162	36	39.1	338	2	F64783	hypothetical prote	235	35	38.0	98	2	C97285	ribosomal protein
163	36	39.1	338	2	S34854	epidermal growth f	236	35	38.0	99	2	S60230	gibberellin-regula
164	36	39.1	338	2	SL0471	CMGL protein - rat	237	35	38.0	111	2	B26567	nitrogen regulator
165	36	39.1	339	2	B39590	TpA-induced protei	238	35	38.0	113	2	AH3371	thioredoxin-disulf
166	36	39.1	394	2	JC4052	aspergillopepsin I	239	35	38.0	117	2	F82589	hypothetical prote
167	36	39.1	394	2	PS0140	aspergillopepsin I	240	35	38.0	129	2	T20081	hypothetical prote
168	36	39.1	394	2	T20778	hypothetical prote	241	35	38.0	181	2	S44765	C29S4.9 protein -
169	36	39.1	406	2	S60962	hypothetical prote	242	35	38.0	186	2	B83491	probable transcrip
170	36	39.1	413	1	VHVN1H	nucleoprotein - in	243	35	38.0	194	2	A55099	muscle LIM protein
171	36	39.1	413	2	T43017	probable prephenat	244	35	38.0	196	2	G83360	probable transcrip
172	36	39.1	425	2	T44592	Atp/GTP-binding pr	245	35	38.0	206	2	AB0727	probable membrane
173	36	39.1	431	2	T41005	prephenate dehydro	246	35	38.0	206	2	C90945	hypothetical prote
174	36	39.1	453	2	D69829	Na+/H+-exchangin	247	35	38.0	206	2	E64943	probable membrane
175	36	39.1	468	2	B40228	neurexin I-beta pr	248	35	38.0	206	2	F85793	hypothetical prote

249	35	38.0	208	2	T16343	hypothetical prote	322	35	38.0	1021	2	H75423	hypothetical prote
250	35	38.0	208	2	WMV912	hypothetical prote	323	35	38.0	1059	2	T12195	sucrose-phosphate
251	35	38.0	230	1	WMV926	p26 protein [simil	324	35	38.0	1095	2	T25520	hypothetical prote
252	35	38.0	248	2	T33230	hypothetical prote	325	35	38.0	1113	2	T20004	hypothetical prote
253	35	38.0	267	2	B72408	conserved hypothet	326	35	38.0	1122	1	FKMUA	phytochrome A - Ar
254	35	38.0	272	2	T08762	hypothetical prote	327	35	38.0	1122	2	D86229	phytochrome A [imp
255	35	38.0	274	2	G70653	hypothetical prote	328	35	38.0	1123	2	S20497	phytochrome A - po
256	35	38.0	295	2	S60711	probable glpQl pro	329	35	38.0	1271	2	T24008	hypothetical prote
257	35	38.0	304	2	B82089	band-6-protein - b	330	35	38.0	1291	2	T13389	hypothetical prote
258	35	38.0	307	2	S16390	transcription regu	331	35	38.0	1338	2	T02206	hypothetical prote
259	35	38.0	320	2	S69547	auxin-induced prot	332	35	38.0	1534	2	T30295	p-glycoprotein - T
260	35	38.0	351	2	A10991	transcription init	333	35	38.0	1534	2	T00415	hypothetical prote
261	35	38.0	363	2	S33702	cell division prot	334	35	38.0	1849	2	C70749	probable ppsa prot
262	35	38.0	366	2	AS2782	homeotic protein D	335	35	38.0	1876	2	T00076	hypothetical prote
263	35	38.0	372	2	AH7562	S-adenosylmethionl	336	34.5	37.5	148	2	S06019	hypothetical prote
264	35	38.0	372	2	A33050	brefeldin A estera	337	34.5	37.5	150	2	C83329	isotocin 2 / neuro
265	35	38.0	382	2	S67770	probable membrane	338	34.5	37.5	154	2	A33896	hypothetical prote
266	35	38.0	383	2	AG3533	spermidine/putresc	339	34.5	37.5	158	2	B34132	isotocin 1 / neuro
267	35	38.0	383	2	A49562	cartilage glycopro	340	34.5	37.5	460	2	C96736	vasotocin / neurop
268	35	38.0	396	1	AMZRB	argininosuccinate	341	34.5	37.5	500	2	T00820	probable ketoacyl -
269	35	38.0	396	2	A97562	S-adenosylmethionl	342	34.5	37.5	573	2	JQ0135	hypothetical prote
270	35	38.0	397	2	C81851	acetylornithine tr	343	34.5	37.5	586	2	S58713	hypothetical 62.8K
271	35	38.0	398	2	H81090	acetylornithine am	344	34.5	37.5	670	2	T43784	probable membrane
272	35	38.0	399	2	B83398	hypothetical prote	345	34.5	37.5	690	2	T27357	NADH2 dehydrogenas
273	35	38.0	402	2	A41594	hypothetical prote	346	34.5	37.5	764	2	T48446	hypothetical prote
274	35	38.0	410	2	AB3546	Na+/H+-exchanging	347	34.5	37.5	851	2	AB3484	hypothetical prote
275	35	38.0	426	2	E95854	aminobutylaldehyde	348	34.5	37.5	1067	2	AB0260	probable heme util
276	35	38.0	430	2	T20551	conserved hypothet	349	34.5	37.5	1104	2	JH0181	probable phase hos
277	35	38.0	445	2	T49318	hypothetical prote	350	34.5	37.5	1168	2	I56985	nitrite reductase
278	35	38.0	449	2	T19554	probable SGP1 prot	351	34	37.0	87	2	T28219	kalinin B1 - mouse
279	35	38.0	454	2	AC0444	hypothetical prote	352	34	37.0	94	2	C59094	hypothetical prote
280	35	38.0	454	2	S61455	probable metabolit	353	34	37.0	111	2	A33600	hypothetical prote
281	35	38.0	467	2	B75322	flagellar hook pro	354	34	37.0	112	2	S74466	nitrogen regulator
282	35	38.0	470	2	T48003	probable oligoend	355	34	37.0	113	2	T44042	photosystem II 13K
283	35	38.0	489	2	H69059	hypothetical prote	356	34	37.0	118	2	T49372	chemokine [improt
284	35	38.0	536	2	B91174	dihydroxy-acid deh	357	34	37.0	128	2	AE3451	hypothetical prote
285	35	38.0	543	2	T32496	hypothetical prote	358	34	37.0	136	2	T46345	hypothetical prote
286	35	38.0	552	2	E90601	hypothetical prote	359	34	37.0	143	2	T49137	hypothetical prote
287	35	38.0	555	2	F70372	hypothetical prote	360	34	37.0	152	1	G25973	pertussis toxin ch
288	35	38.0	557	2	S24395	dihydroxyacid dehy	361	34	37.0	171	2	E84773	hypothetical prote
289	35	38.0	580	2	B86020	protein-tyrosine-p	362	34	37.0	208	2	F75355	3-isopropylmalate
290	35	38.0	587	2	A36347	hypothetical prote	363	34	37.0	209	2	T39652	probable DNA J dom
291	35	38.0	569	2	S41200	glypican 1 precura	364	34	37.0	221	2	C84899	hypothetical prote
292	35	38.0	573	2	C84645	phosphoglucutase	365	34	37.0	222	2	E97526	hypothetical prote
293	35	38.0	627	2	T19542	hypothetical prote	366	34	37.0	239	2	G72400	30S ribosomal prot
294	35	38.0	630	2	F86317	hypothetical prote	367	34	37.0	245	2	F69343	16S pseudouridyat
295	35	38.0	642	2	T51421	protein F15H18.17	368	34	37.0	252	2	T45737	2-oxoacid-ferredox
296	35	38.0	648	2	S50856	L-aspartate oksidas	369	34	37.0	255	2	AE2745	hypothetical prote
297	35	38.0	654	2	T34613	whn protein - rat	370	34	37.0	255	2	E82363	30S ribosomal prot
298	35	38.0	657	2	G97658	NADH2 dehydrogenas	371	34	37.0	265	1	CTBOP	conserved hypothet
299	35	38.0	699	2	F97721	hypothetical prote	372	34	37.0	268	2	S39711	corticotropin / li
300	35	38.0	699	2	B71723	elongation factor	373	34	37.0	268	2	B61615	ywDF protein - Bac
301	35	38.0	700	2	T20550	translation elonga	374	34	37.0	279	2	T34860	fibroin heavy chai
302	35	38.0	701	2	S31150	hypothetical prote	375	34	37.0	292	2	E72208	probable oxidoredu
303	35	38.0	701	2	H87143	translation elonga	376	34	37.0	296	2	D70314	conserved hypothet
304	35	38.0	702	2	E0827	elongation factor	377	34	37.0	315	2	H81907	heme O oxygenase -
305	35	38.0	730	2	S24376	probable fusa1 prot	378	34	37.0	315	2	F81107	probable periplasm
306	35	38.0	737	2	T46101	2-aminobenzoyl-CoA	379	34	37.0	317	2	D89961	stomatatin/Mec-2 fam
307	35	38.0	747	2	S46608	ABC transporter-li	380	34	37.0	319	2	B82951	conserved hypothet
308	35	38.0	755	2	A13228	VTall protein - ye	381	34	37.0	320	2	B87135	conserved hypothet
309	35	38.0	804	2	T05783	tryptophan 2-monoo	382	34	37.0	322	1	F64360	conserved hypothet
310	35	38.0	815	2	JG0197	hypothetical prote	383	34	37.0	324	2	T15744	hypothetical prote
311	35	38.0	832	2	B96702	myosin-light-chain	384	34	37.0	327	2	A48804	afatoxin B1 aldeh
312	35	38.0	857	2	B82290	hypothetical prote	385	34	37.0	329	2	T32578	hypothetical prote
313	35	38.0	865	1	ISRCTP	clpB protein VC071	386	34	37.0	341	2	T20517	hypothetical prote
314	35	38.0	865	2	AF0654	DNA topoisomerase	387	34	37.0	342	2	T02669	hypothetical prote
315	35	38.0	865	2	F90859	DNA topoisomerase	388	34	37.0	352	2	E81255	two-component syst
316	35	38.0	888	2	A85760	DNA topoisomerase	389	34	37.0	355	2	AE0426	probable aspartate
317	35	38.0	901	2	T51593	GTP-binding regula	390	34	37.0	357	2	T29856	ct474 hypothetical
318	35	38.0	910	2	T01135	probable GTP-bind	391	34	37.0	362	2	A72061	conserved hypothet
319	35	38.0	924	2	T22050	hypothetical prote	392	34	37.0	362	2	D81606	conserved hypothet
320	35	38.0	1001	2	T22044	hypothetical prote	393	34	37.0	364	2	F86564	CT474 hypothetical
321	35	38.0	1018	2	AG2556	G9a protein - huma	394	34	37.0	364	2	D75539	branched-chain ami

395	34	37.0	367	2	J6C087	468	34	37.0	830	2	T19283	hypothetical prote
396	34	37.0	372	2	JC2556	469	34	37.0	837	2	A57542	p96 protein - mous
397	34	37.0	372	2	A82016	470	34	37.0	880	2	T18771	probable chloride
398	34	37.0	374	2	S69627	471	34	37.0	888	2	D84824	probable DNA-direc
399	34	37.0	375	2	D97268	472	34	37.0	892	2	T09071	SH3 domains-contai
400	34	37.0	393	2	S67050	473	34	37.0	903	2	T00074	hypothetical prote
401	34	37.0	397	1	Z68PT9	474	34	37.0	907	2	F84825	hypothetical prote
402	34	37.0	397	2	D96987	475	34	37.0	1022	1	I39643	RFX-toxin I - Acti
403	34	37.0	403	2	A82423	476	34	37.0	1027	2	C86300	protein F309.28 [i
404	34	37.0	415	2	F91209	477	34	37.0	1035	2	T16588	hypothetical prote
405	34	37.0	415	2	A86056	478	34	37.0	1057	2	T16676	hypothetical prote
406	34	37.0	415	2	A39412	479	34	37.0	1060	2	T30347	vitellogenin conve
407	34	37.0	419	2	S22136	480	34	37.0	1157	2	F97255	fusion of alpha-gl
408	34	37.0	425	2	JC6557	481	34	37.0	1217	2	E97177	alpha-glucosidase
409	34	37.0	437	1	A48061	482	34	37.0	1229	2	S14159	probable adenylate
410	34	37.0	437	1	S50853	483	34	37.0	1298	2	I54367	X-linked nuclear p
411	34	37.0	437	2	A64891	484	34	37.0	1328	1	S04273	retrovirus-related
412	34	37.0	438	2	D84331	485	34	37.0	1458	2	A45665	adult-specific bru
413	34	37.0	445	2	T37161	486	34	37.0	1547	2	A12043	hypothetical prote
414	34	37.0	456	2	C86624	487	34	37.0	1641	2	I38614	helicase II - huma
415	34	37.0	456	2	H72000	488	34	37.0	1722	2	I78879	reinoblastoma bin
416	34	37.0	457	2	E82714	489	34	37.0	1729	2	A49282	fusion protein Ia/
417	34	37.0	459	2	F81914	490	34	37.0	1888	2	T39009	hypothetical prote
418	34	37.0	459	2	G81187	491	34	37.0	2109	1	I50421	aggreacan precursor
419	34	37.0	459	2	G70672	492	34	37.0	3759	2	A35085	trithorax protein
420	34	37.0	465	2	E87591	493	34	37.0	3828	2	T13857	trithorax protein
421	34	37.0	466	2	AC2696	494	33.5	36.4	78	2	C90872	hypothetical prote
422	34	37.0	466	2	C97478	495	33.5	36.4	153	2	A34132	vasotocin / neuroph
423	34	37.0	480	2	T33809	496	33.5	36.4	159	2	JC1489	isotocin-I neuroph
424	34	37.0	483	2	A25896	497	33.5	36.4	159	2	I51077	isotocin-I precurs
425	34	37.0	495	2	F89818	498	33.5	36.4	491	2	T08996	ribulose-1,5-bisph
426	34	37.0	500	2	F88921	499	33.5	36.4	495	2	T08995	ribulose-1,5-bisph
427	34	37.0	501	2	G83848	500	33.5	36.4	631	2	AD2224	hypothetical prote
428	34	37.0	503	2	B83772	501	33.5	36.4	642	2	B49849	terminase large ch
429	34	37.0	509	2	S49349	502	33.5	36.4	1091	2	T34247	hypothetical prote
430	34	37.0	533	2	AG2328	503	33.5	36.4	1107	2	J34246	hypothetical prote
431	34	37.0	534	2	H69056	504	33	35.9	45	2	J30655	hypothetical 5K pr
432	34	37.0	546	2	I48899	505	33	35.9	52	2	D82517	hypothetical prote
433	34	37.0	550	2	A48063	506	33	35.9	75	2	G89976	conserved hypotet
434	34	37.0	550	2	I45067	507	33	35.9	78	2	E84605	conserved hypotet
435	34	37.0	553	2	T423571	508	33	35.9	80	2	E83102	hypothetical prote
436	34	37.0	559	2	T41199	509	33	35.9	115	2	T07576	hypothetical prote
437	34	37.0	586	2	T21683	510	33	35.9	117	2	G70127	hypothetical prote
438	34	37.0	588	1	VXAGCA	511	33	35.9	123	2	S47709	hypothetical 14.2K
439	34	37.0	591	2	B83457	512	33	35.9	125	1	R3EG12	ribosomal protein
440	34	37.0	594	1	A56684	513	33	35.9	131	1	WBER41	percutiss toxin ch
441	34	37.0	594	2	T34855	514	33	35.9	131	2	H64788	ybcy protein - Esc
442	34	37.0	598	2	E97686	515	33	35.9	143	2	H90835	hypothetical prote
443	34	37.0	598	2	AG2911	516	33	35.9	145	2	T20956	hypothetical prote
444	34	37.0	608	1	NCECXF	517	33	35.9	149	2	T04083	probable ribosomal
445	34	37.0	608	2	F85933	518	33	35.9	152	1	H25973	percutiss toxin ch
446	34	37.0	608	2	D91088	519	33	35.9	163	2	F83936	hypothetical prote
447	34	37.0	611	2	AI0864	520	33	35.9	164	2	A87556	hypothetical prote
448	34	37.0	612	2	T18848	521	33	35.9	166	2	E90471	hypothetical prote
449	34	37.0	626	1	A48648	522	33	35.9	167	2	C84773	hypothetical prote
450	34	37.0	643	2	T43052	523	33	35.9	170	2	D90959	probable tail tube
451	34	37.0	652	2	AE0125	524	33	35.9	170	2	F85807	probable tail tube
452	34	37.0	658	2	H95952	525	33	35.9	173	1	QQMX2	probable transcrip
453	34	37.0	664	1	B32243	526	33	35.9	173	2	F88535	protein B0523.3 [i
454	34	37.0	665	2	T00015	527	33	35.9	176	2	B75430	transcription regu
455	34	37.0	680	2	S63895	528	33	35.9	181	2	B75430	hypothetical prote
456	34	37.0	680	2	E85431	529	33	35.9	188	2	C84787	hypothetical prote
457	34	37.0	703	2	D71420	530	33	35.9	190	2	S38906	hypothetical prote
458	34	37.0	704	2	B83914	531	33	35.9	190	2	T31661	hypothetical prote
459	34	37.0	717	2	H85171	532	33	35.9	197	2	S44735	b0523.3 protein -
460	34	37.0	719	2	T09543	533	33	35.9	206	2	AH0259	probable phage tai
461	34	37.0	722	2	F87662	534	33	35.9	211	2	F97113	probable nucleotid
462	34	37.0	727	2	AD2188	535	33	35.9	213	2	T18684	hypothetical prote
463	34	37.0	739	2	T52289	536	33	35.9	213	2	D89351	protein F14H3.6 [i
464	34	37.0	748	2	A64319	537	33	35.9	220	2	T03967	RAB24 protein - ri
465	34	37.0	772	2	T16474	538	33	35.9	221	2	C69505	CDPdiacylglycerol -
466	34	37.0	774	2	F96639	539	33	35.9	222	2	B85694	unknown protein en
467	34	37.0	809	2	T20430	540	33	35.9	242	2	B96571	hypothetical prote
									244	2	T02511	DREB-like AP2 doma

541	33	35.9	245	2	T20931	hypothetical prote	614	33	35.9	446	2	AD0509	citrate-sodium sym
542	33	35.9	246	2	S51970	hypothetical prote	615	33	35.9	446	2	B42661	citrate carrier pr
543	33	35.9	247	2	A70910	probable truncated	616	33	35.9	446	2	G86673	NADH oxidase noxe
544	33	35.9	250	2	H96669	protein FIN19.25 l	617	33	35.9	447	2	S76321	histidine-tRNA lig
545	33	35.9	253	2	S65170	hypothetical prote	618	33	35.9	452	2	B90640	D-alanine D-alanin
546	33	35.9	254	2	B72549	hypothetical prote	619	33	35.9	452	2	P64730	UDP-N-acetylmuramo
547	33	35.9	258	2	A33953	enterotoxin D prec	620	33	35.9	452	2	B85491	D-alanine-D-alanin
548	33	35.9	258	2	H83373	hypothetical prote	621	33	35.9	452	2	H88337	protein FlsA4.1 [i
549	33	35.9	260	2	S81384	fumarate reductase	622	33	35.9	453	2	AF1371	aspartate kinase h
550	33	35.9	262	2	S65524	probable transcrip	623	33	35.9	453	2	AD1741	aspartate kinase h
551	33	35.9	267	2	H97155	probable rRNA meth	624	33	35.9	455	2	T23712	hypothetical prote
552	33	35.9	270	2	AD1409	hydrolase (esteras	625	33	35.9	460	2	T45968	hypothetical prote
553	33	35.9	270	2	T24529	hypothetical prote	626	33	35.9	462	2	A86717	conserved hypoteth
554	33	35.9	275	2	H69843	hypothetical prote	627	33	35.9	467	2	I50476	keratin type I - g
555	33	35.9	281	2	E71046	probable ferredoxi	628	33	35.9	470	2	G70870	hypothetical prote
556	33	35.9	281	2	G75168	2-ketoglutarate fe	629	33	35.9	470	2	B72567	hypothetical prote
557	33	35.9	281	2	D82154	hypothetical prote	630	33	35.9	473	2	B84143	Na+/H+ antiporter
558	33	35.9	291	2	E81890	hypothetical prote	631	33	35.9	474	2	E85175	ATP-dependent RNA
559	33	35.9	291	2	H81132	hypothetical prote	632	33	35.9	478	2	A72721	probable Glycerol
560	33	35.9	298	1	D69023	cell division inhi	633	33	35.9	479	2	AF3019	pyruvate kinase [i
561	33	35.9	299	2	AC2998	glutamyl-tRNA synt	634	33	35.9	479	2	C98265	pyruvate kinase (P
562	33	35.9	299	2	F90285	transcription regu	635	33	35.9	483	2	T51272	hypothetical prote
563	33	35.9	306	2	B96922	probable membrane	636	33	35.9	484	2	S62938	hypothetical prote
564	33	35.9	308	2	AC1053	coxin M1-1 precurs	637	33	35.9	488	2	D35385	hydrogen dehydroge
565	33	35.9	316	1	NJ3YMI	methionyl-tRNA for	638	33	35.9	505	2	AD0511	probable carnitine
566	33	35.9	319	2	E86861	two-component sens	639	33	35.9	508	2	S74977	hypothetical prote
567	33	35.9	320	2	F69747	hypothetical prote	640	33	35.9	509	2	JH0501	zinc finger protei
568	33	35.9	321	2	T32320	conserved hypoteth	641	33	35.9	510	2	A96735	hypothetical prote
569	33	35.9	322	1	D69999	phosphotriestrase	642	33	35.9	512	1	O4HU6	aryl hydrocarbon (
570	33	35.9	325	2	A28214	glycerol-3-phospha	643	33	35.9	512	2	F85342	beta-1,3-glucanas
571	33	35.9	327	2	AI2901	probable glycerol-	644	33	35.9	513	1	R85CAY	transcription regu
572	33	35.9	327	2	C97677	hypothetical prote	645	33	35.9	513	2	F90866	hypothetical prote
573	33	35.9	329	2	A63776	probable arAC-fam1	646	33	35.9	513	2	C85752	probable flavoprot
574	33	35.9	334	2	T36485	hypothetical prote	647	33	35.9	517	2	T37806	uroporphyrinogen I
575	33	35.9	339	2	C84653	hypothetical prote	648	33	35.9	518	2	AC2237	cytochrome P450 1A
576	33	35.9	340	2	H64717	sialoglycoproteina	649	33	35.9	521	2	A27821	cytochrome P450 1A
577	33	35.9	340	2	E71801	probable O-sialogl	650	33	35.9	521	2	S55318	cytochrome P450 1A
578	33	35.9	341	2	S72649	sucrose-phosphate	651	33	35.9	521	2	S55317	cytochrome P450 1A
579	33	35.9	351	2	H84847	probable protein k	652	33	35.9	521	2	S34184	cytochrome P450 1A
580	33	35.9	357	1	G69290	probable hexosyltr	653	33	35.9	524	1	O4RTMC	unspecific monooxy
581	33	35.9	363	2	T24809	hypothetical prote	654	33	35.9	524	2	T31311	lysine-tRNA ligase
582	33	35.9	367	2	T17481	prephenate dehydro	655	33	35.9	527	2	S64702	cell surface antig
583	33	35.9	370	2	S54297	protein phosphatas	656	33	35.9	530	2	S53392	probable membrane
584	33	35.9	373	2	A96927	probable N6-adenin	657	33	35.9	535	2	A87570	ABC transporter, A
585	33	35.9	375	2	H98185	membrane dipeptida	658	33	35.9	536	2	A34596	transcription fact
586	33	35.9	375	2	AB3101	dipeptidase [impor	659	33	35.9	537	1	YRHUB6	tyrosinase-related
587	33	35.9	376	2	AC0440	probable oxidoredu	660	33	35.9	541	2	T34850	probable acid-CoA
588	33	35.9	378	2	A97552	Chain A, crystal s	661	33	35.9	544	2	E75569	probable aminotran
589	33	35.9	394	2	G86190	hypothetical prote	662	33	35.9	558	2	T21468	hypothetical prote
590	33	35.9	394	2	S42751	asparillopepsin I	663	33	35.9	560	2	T32288	hypothetical prote
591	33	35.9	394	2	T40897	hypothetical prote	664	33	35.9	561	2	C64459	dihydroxy-acid deh
592	33	35.9	397	2	D69538	arsenite transport	665	33	35.9	572	2	T51575	2-hydroxyphytanoyl
593	33	35.9	398	2	S44028	actin-related prot	666	33	35.9	575	2	C34106	protein kinase (EC
594	33	35.9	403	2	G82831	queine tRNA-fibos	667	33	35.9	581	2	B81107	exodeoxyribonuclea
595	33	35.9	405	2	T43023	ceoA protein - Bur	668	33	35.9	581	2	B81909	exodeoxyribonuclea
596	33	35.9	409	2	A84606	hypothetical prote	669	33	35.9	589	2	S42385	hypothetical prote
597	33	35.9	411	2	H64048	hypothetical prote	670	33	35.9	590	2	F75501	sensor histidine k
598	33	35.9	411	2	AD0039	UV protection prot	671	33	35.9	599	2	T48383	uracil transporter
599	33	35.9	413	2	E81984	pilin glycosylatio	672	33	35.9	609	2	E82423	hypothetical prote
600	33	35.9	413	2	E81039	pilin glycosylatio	673	33	35.9	614	2	D34106	protein kinase (EC
601	33	35.9	414	1	I38977	TAR DNA-binding pr	674	33	35.9	625	2	G97076	alkaline phosphata
602	33	35.9	418	2	S29506	neurotensin recept	675	33	35.9	634	2	JC7808	delta-glutamate re
603	33	35.9	421	2	A71345	probable phosphori	676	33	35.9	641	2	T03095	homoprotein Sail
604	33	35.9	425	2	AD2655	3-phosphoshikimate	677	33	35.9	645	2	F70825	probable PPE prote
605	33	35.9	425	2	H97436	3-phosphoshikimate	678	33	35.9	652	2	B84686	hypothetical prote
606	33	35.9	425	2	AD3039	replication protei	679	33	35.9	653	2	T12482	hypothetical prote
607	33	35.9	428	2	H98246	probable replicati	680	33	35.9	662	2	D40228	neurexin II-beta p
608	33	35.9	429	2	T05011	hypothetical prote	681	33	35.9	667	2	F87291	methyl-accepting c
609	33	35.9	430	2	H97013	probable membrane	682	33	35.9	668	2	B66740	hypothetical prote
610	33	35.9	431	2	C87436	major facilitator	683	33	35.9	680	2	S63698	NADPH-ferrihemopro
611	33	35.9	441	2	C69834	sensory transducti	684	33	35.9	680	2	A37890	NADPH-ferrihemopro
612	33	35.9	445	2	F71265	probable NADH oxid	685	33	35.9	695	2	A37890	hypothetical prote
613	33	35.9	446	2	A42661	citrate carrier pr	686	33	35.9	695	2	T46113	hypothetical prote

687	33	35.9	701	2	C26956	translation elonga	760	33	35.9	2670	2	A46719	inositol 1,4,5-tri
688	33	35.9	701	2	T28151	probable ABC-type	761	33	35.9	2671	2	A49873	inositol 1,4,5-tri
689	33	35.9	705	2	S54521	probable membrane	762	33	35.9	3178	2	S13595	6-deoxyerythronoi
690	33	35.9	713	2	G84586	hypothetical prote	763	33	35.9	3712	2	S18253	laminin alpha-1 ch
691	33	35.9	720	2	G97229	pullulanase [impor	764	33	35.9	3947	2	T52486	ferrichrome sidero
692	33	35.9	747	1	A57107	kinesin-related pr	765	32.5	35.3	40	2	S21748	probable lipid tra
693	33	35.9	747	2	T42599	minor capsid prote	766	32.5	35.3	93	2	A60357	neurophysin 1 - go
694	33	35.9	750	2	T21534	hypothetical prote	767	32.5	35.3	264	2	T36431	probable ABC-type
695	33	35.9	753	1	WZBEE8	gene 56 protein -	768	32.5	35.3	323	2	AB1659	hypothetical prote
696	33	35.9	763	2	A69440	alpha-glucosidase	769	32.5	35.3	342	2	T45456	probable membrane
697	33	35.9	765	2	D86335	conserved hypotet	770	32.5	35.3	376	2	S40470	mitogen-activated
698	33	35.9	769	2	D86335	T2OH2.6 protein -	771	32.5	35.3	379	2	G75294	zinc metallohydrol
699	33	35.9	779	2	A57177	NIMA-like protein	772	32.5	35.3	384	2	G96689	probable fructokin
700	33	35.9	780	2	T03156	ribonucleoside-dip	773	32.5	35.3	453	2	UQ0766	phenylalanine 4-mo
701	33	35.9	782	2	I58376	hypothetical prote	774	32.5	35.3	455	2	T00856	pectate lyase (EC
702	33	35.9	798	2	A69979	conjugation trans	775	32.5	35.3	581	2	S53105	pectinesterase pre
703	33	35.9	798	2	AE1263	exodeoxyribonuclea	776	32.5	35.3	614	2	F86719	hypothetical prote
704	33	35.9	798	2	AG1625	exodeoxyribonuclea	777	32.5	35.3	633	2	T02686	probable Ser/Thr p
705	33	35.9	802	2	G96640	hypothetical prote	778	32.5	35.3	638	2	AC1123	B. subtilis Iold p
706	33	35.9	804	2	AG1038	conserved hypotet	779	32.5	35.3	638	2	AE1483	hypothetical prote
707	33	35.9	809	2	S40460	ribosomal protein	780	32.5	35.3	718	2	T29448	probable peroxidase
708	33	35.9	817	2	A96640	protein Tif9.2 [im	781	32.5	35.3	724	2	T27858	hypothetical prote
709	33	35.9	820	2	G86246	hypothetical prote	782	32.5	35.3	808	2	T23129	hypothetical prote
710	33	35.9	823	2	G89007	protein F59B1.8 [i	783	32.5	35.3	836	2	B96716	probable serine/th
711	33	35.9	828	2	S34695	hypothetical prote	784	32.5	35.3	915	1	WMBEV3	ribonucleoside-dip
712	33	35.9	829	2	B96640	hypothetical prote	785	32.5	35.3	1220	2	AD0125	exodeoxyribonuclea
713	33	35.9	831	2	D96639	protein Tif9.12 [i	786	32.5	35.3	1395	2	T00068	hypothetical prote
714	33	35.9	848	2	E85087	hypothetical prote	787	32	34.8	70	2	G45186	homeotic protein G
715	33	35.9	887	1	WZBEE5	gene 53 protein -	788	32	34.8	81	1	T5EP2A	short toxin 2 prec
716	33	35.9	892	2	T50985	related to transcr	789	32	34.8	81	2	B90344	hypothetical prote
717	33	35.9	901	2	T04108	receptor kinase ho	790	32	34.8	101	2	D82219	PTS system, cellob
718	33	35.9	901	2	JC6093	dead ringer nuclea	791	32	34.8	101	2	C84023	hypothetical prote
719	33	35.9	912	2	T01769	hypothetical prote	792	32	34.8	105	2	S23061	hypothetical prote
720	33	35.9	912	2	S74860	DNA mismatch repa	793	32	34.8	117	2	G85690	minor capsid prote
721	33	35.9	934	2	T08418	protein kinase (EC	794	32	34.8	117	2	E90833	hypothetical prote
722	33	35.9	944	2	S26710	spindle pole body	795	32	34.8	122	2	S74818	glycine-rich prote
723	33	35.9	949	2	T03030	hypothetical prote	796	32	34.8	129	2	T03861	NADH ubiquinone ox
724	33	35.9	953	2	S54478	probable membrane	797	32	34.8	133	2	JC2003	probable DNA-bind
725	33	35.9	965	2	S62935	hypothetical prote	798	32	34.8	134	2	AD0618	conserved hypotet
726	33	35.9	971	2	T19431	hypothetical prote	799	32	34.8	134	2	AH2645	hypothetical prote
727	33	35.9	979	2	B86207	hypothetical prote	800	32	34.8	135	2	G72523	probable membrane
728	33	35.9	993	2	A96750	hypothetical prote	801	32	34.8	136	2	AC0599	hypothetical prote
729	33	35.9	1002	2	T02488	hypothetical prote	802	32	34.8	139	2	T28849	hypothetical prote
730	33	35.9	1007	2	T32285	hypothetical prote	803	32	34.8	140	2	E64364	ribosomal protein
731	33	35.9	1091	2	G64964	hypothetical prote	804	32	34.8	145	2	S41193	hypothetical prote
732	33	35.9	1096	1	S61917	protein kinase C (805	32	34.8	145	2	H97427	homeotic protein H
733	33	35.9	1108	2	T31335	hglC protein - Ana	806	32	34.8	153	1	WJHU3C	homeotic protein H
734	33	35.9	1109	2	AC2475	heterocyst glycoli	807	32	34.8	153	1	WJMSX6	probable mucR fami
735	33	35.9	1127	2	S47445	MDM1 protein - yea	808	32	34.8	154	2	F95311	hypothetical prote
736	33	35.9	1139	2	T23018	hypothetical prote	809	32	34.8	154	2	F72741	hypothetical prote
737	33	35.9	1156	2	D84639	probable retroelem	810	32	34.8	155	2	A85582	probable endopepti
738	33	35.9	1178	2	AC3394	DNA-directed DNA p	811	32	34.8	155	2	D90731	probable endopepti
739	33	35.9	1203	2	D86625	subunit A of ATP-d	812	32	34.8	159	2	S20143	hypothetical prote
740	33	35.9	1215	2	S50428	probable Ca2+-tran	813	32	34.8	159	2	T09852	hypothetical prote
741	33	35.9	1254	2	JC7185	chromosome 1 Clorf	814	32	34.8	159	2	A85022	probable actin pol
742	33	35.9	1349	2	T13031	nucleoporin - frui	815	32	34.8	164	2	T24272	hypothetical prote
743	33	35.9	1354	2	AG0538	Rhs-family protein	816	32	34.8	165	2	S28020	pepidylprolyl iso
744	33	35.9	1363	1	VGHF1	E2 glycoprotein pr	817	32	34.8	166	2	G87423	ferredoxin, probab
745	33	35.9	1363	2	S44241	surface protein -	818	32	34.8	168	2	S78110	thi protein - Rhiz
746	33	35.9	1365	2	T13391	nucleoporin 154 -	819	32	34.8	174	2	T29801	hypothetical prote
747	33	35.9	1374	2	AE3259	extracellular seri	820	32	34.8	178	2	C83705	hypothetical prote
748	33	35.9	1375	2	T30813	plasmaenogen relate	821	32	34.8	178	2	C83408	hypothetical prote
749	33	35.9	1415	2	A72369	(R)-2-hydroxygluta	822	32	34.8	181	2	C97709	cdp-diacylglycerol
750	33	35.9	1423	1	S27941	serum albumin - se	823	32	34.8	181	2	A71713	hypothetical prote
751	33	35.9	1571	2	AC1647	Lactobacillus phag	824	32	34.8	181	2	T05301	hypothetical prote
752	33	35.9	1607	2	T21582	hypothetical prote	825	32	34.8	181	2	F83907	hypothetical prote
753	33	35.9	1715	2	C40228	neurexin II-alpha	826	32	34.8	186	2	E71335	probable cytidylat
754	33	35.9	1797	2	A55677	laminin beta-2 cha	827	32	34.8	188	2	C87341	conserved hypotet
755	33	35.9	1848	2	A44140	cellulose-binding	828	32	34.8	194	2	S57472	murine muscle LIM
756	33	35.9	1896	2	B72175	D15R protein - var	829	32	34.8	197	2	F70423	hypothetical prote
757	33	35.9	1897	2	T28621	hypothetical prote	830	32	34.8	202	2	S22499	hypothetical prote
758	33	35.9	1959	1	AGRT	agrin - rat	831	32	34.8	203	2	T29844	hypothetical prote
759	33	35.9	2054	2	T07584	hypothetical prote	832	32	34.8	203	2	JQ0853	hypothetical 22.9K

833	32	34.8	206	2	T25139	hypothetical prote	906	32	34.8	351	2	D97422	probable methylest
834	32	34.8	213	2	S72625	hypothetical prote	907	32	34.8	351	2	AC2640	protein-glutamate
835	32	34.8	215	2	C37273	membrane glycoprot	908	32	34.8	351	2	S29979	hype protein - Alc
836	32	34.8	217	2	I67410	somatotropin - rhe	909	32	34.8	352	1	CBCEFX	cell division prot
837	32	34.8	217	2	T37859	probable transcript	910	32	34.8	352	2	AB2248	N-acetyl-glutamate
838	32	34.8	218	2	S60285	B15C protein - bar	911	32	34.8	352	2	G91167	cell division memb
839	32	34.8	219	2	A70314	deoxyribose-phosph	912	32	34.8	352	2	G86013	cell division memb
840	32	34.8	227	2	D71312	probable Holliday	913	32	34.8	353	2	S33322	(S)-2-hydroxy-acid
841	32	34.8	230	1	QJ1749	E1 membrane glycop	914	32	34.8	356	2	S71179	cinnamyl-alcohol d
842	32	34.8	233	2	A69004	CDPdiacylglycerol -	915	32	34.8	357	2	S29275	hypothetical prote
843	32	34.8	234	1	S02014	homeotic protein H	916	32	34.8	359	2	JC5277	G protein-coupled
844	32	34.8	234	2	S00992	homeotic protein H	917	32	34.8	360	2	T08581	cinnamyl-alcohol d
845	32	34.8	235	2	B84393	phosphoserine phos	918	32	34.8	360	2	F70045	two-component sens
846	32	34.8	235	2	S74229	homeotic protein H	919	32	34.8	363	2	T05624	cinnamyl-alcohol d
847	32	34.8	235	2	A56568	homeotic protein H	920	32	34.8	369	2	G71515	probable (cbs doma
848	32	34.8	238	2	AE2027	hypothetical prote	921	32	34.8	370	2	G83513	conserved hypotet
849	32	34.8	239	2	T39283	hypothetical prote	922	32	34.8	372	2	AE2613	DNA polymerase III
850	32	34.8	245	2	D87600	3-oxoacyl-(acyl-ca	923	32	34.8	373	2	E70864	probable oxidoredu
851	32	34.8	247	2	T31204	hypothetical prote	924	32	34.8	383	2	E84249	3-ketoacyl-CoA thi
852	32	34.8	250	2	T45893	hypothetical prote	925	32	34.8	385	2	G97350	xylR transcription
853	32	34.8	250	2	S56807	hypothetical prote	926	32	34.8	387	2	B75981	magnesium/cobalt t
854	32	34.8	252	2	E83612	conserved hypotet	927	32	34.8	387	2	B82891	ferrichrome transp
855	32	34.8	255	2	S04105	myogenic factor 5	928	32	34.8	397	2	S76786	DNA polymerase III
856	32	34.8	260	2	B53422	peptidylprolyl iso	929	32	34.8	403	2	C97395	hypothetical prote
857	32	34.8	262	2	H83214	probable permease	930	32	34.8	404	2	T30231	cytochrome P450 -
858	32	34.8	266	2	D87265	hypothetical prote	931	32	34.8	404	2	A37234	exo-alpha-sialidas
859	32	34.8	271	2	B86918	hypothetical prote	932	32	34.8	407	2	AE1599	conserved hypotet
860	32	34.8	272	2	T15889	hypothetical prote	933	32	34.8	408	2	T01006	hypothetical prote
861	32	34.8	276	2	T00923	hypothetical prote	934	32	34.8	409	2	AG2869	N-carbamoyl-beta-a
862	32	34.8	281	2	AH3012	outer surface prot	935	32	34.8	409	2	T03001	probable integrase
863	32	34.8	282	2	A47795	probable transcript	936	32	34.8	410	2	E96729	unknown protein F5
864	32	34.8	284	2	G98271	hypothetical prote	937	32	34.8	411	2	T01388	oxidoreductase hom
865	32	34.8	286	2	H69470	diptetide ABC tran	938	32	34.8	412	2	F64849	probable permease
866	32	34.8	287	2	B95326	AttB-like ABC tran	939	32	34.8	412	2	C99809	hypothetical prote
867	32	34.8	288	2	AD2010	hypothetical prote	940	32	34.8	412	2	G85668	hypothetical prote
868	32	34.8	287	2	T38075	conserved hypotet	941	32	34.8	414	2	A64504	hypothetical prote
869	32	34.8	291	2	B71333	conserved hypotet	942	32	34.8	415	2	A97646	n-carbamoyl-beta-a
870	32	34.8	291	2	H83340	hypothetical prote	943	32	34.8	417	2	I50407	phosphoglycerate k
871	32	34.8	295	2	E75466	hypothetical prote	944	32	34.8	420	1	DCECD	diaminopimelate de
872	32	34.8	297	2	H75132	hypothetical prote	945	32	34.8	420	2	B85936	diaminopimelate de
873	32	34.8	297	2	T45436	hypothetical membr	946	32	34.8	420	2	G91090	diaminopimelate de
874	32	34.8	299	2	S53395	hypothetical prote	947	32	34.8	422	2	T51199	hypothetical prote
875	32	34.8	300	1	B71090	hypothetical prote	948	32	34.8	425	2	A98152	sensor histidine k
876	32	34.8	301	2	S60936	LEE1 protein - yea	949	32	34.8	427	2	F85436	hypothetical prote
877	32	34.8	306	2	T47832	hypothetical prote	950	32	34.8	429	2	T31001	hypothetical prote
878	32	34.8	308	2	D71353	hypothetical prote	951	32	34.8	431	2	S50633	hypothetical prote
879	32	34.8	308	2	T46023	hypothetical prote	952	32	34.8	436	2	AH2442	hypothetical prote
880	32	34.8	308	1	E65112	hypothetical 34.6	953	32	34.8	438	2	B97111	probable GTPase li
881	32	34.8	309	2	AH0906	conserved hypotet	954	32	34.8	440	2	S37303	sox-4 protein mo
882	32	34.8	309	2	E85985	hypothetical prote	955	32	34.8	442	2	H86276	F14I17.4 protein -
883	32	34.8	309	2	B91140	hypothetical prote	956	32	34.8	450	2	S66942	probable membrane
884	32	34.8	312	1	S22397	pyruvate synthase	957	32	34.8	452	2	AC3136	two component sens
885	32	34.8	312	2	E84268	hypothetical prote	958	32	34.8	454	1	A45340	nucleocapsid prote
886	32	34.8	313	2	B86908	probable esterase	959	32	34.8	454	1	A45396	nucleocapsid prote
887	32	34.8	314	2	E86928	hypothetical prote	960	32	34.8	454	1	B45340	nucleocapsid prote
888	32	34.8	315	2	B96685	34 kDa antigen lim	961	32	34.8	454	1	C45340	nucleocapsid prote
889	32	34.8	315	2	B96685	hypothetical prote	962	32	34.8	455	1	D45340	nucleocapsid prote
890	32	34.8	316	2	T27194	hypothetical prote	963	32	34.8	455	1	VH1HMJ	nucleocapsid prote
891	32	34.8	321	2	AE1282	conserved hypotet	964	32	34.8	456	2	B96688	unknown protein, 1
892	32	34.8	321	2	A11653	conserved hypotet	965	32	34.8	464	2	T50785	nucleoid DNA-bind
893	32	34.8	323	2	AC2481	hypothetical prote	966	32	34.8	465	2	T27032	hypothetical prote
894	32	34.8	324	1	A48953	chologylglycine hyd	967	32	34.8	489	2	T39038	hypothetical prote
895	32	34.8	325	2	D84060	hypothetical prote	968	32	34.8	495	2	A95984	probable xanthine
896	32	34.8	326	2	B71602	probable secreted	969	32	34.8	498	2	T20646	hypothetical prote
897	32	34.8	326	2	A33755	myb-induced myeloi	970	32	34.8	498	2	H83793	hypothetical prote
898	32	34.8	327	2	C97057	spore protease lim	971	32	34.8	498	2	H71279	probable femA prot
899	32	34.8	330	2	E95362	probable Arac-fam1	972	32	34.8	500	2	T20869	hypothetical prote
900	32	34.8	335	2	E81278	probable glycoprot	973	32	34.8	503	2	T30966	hypothetical prote
901	32	34.8	337	1	A35260	alcohol dehydrogen	974	32	34.8	506	2	D96672	probable Cytochrom
902	32	34.8	337	2	S31131	hypothetical prote	975	32	34.8	509	2	B84643	hypothetical prote
903	32	34.8	340	2	B97011	probably O-sialogl	976	32	34.8	510	2	A96673	probable cytochrom
904	32	34.8	340	2	F88545	protein F59B2.111	977	32	34.8	511	2	G96672	hypothetical prote
905	32	34.8	345	2	T01348	hypothetical prote	978	32	34.8	511	2	H96672	probable cytochrom

979 32 34.8 511 2 T46865 phosphoglycerate m
980 32 34.8 512 2 E84501 probable cytochrom
981 32 34.8 514 2 A49838 site-specific reco
982 32 34.8 514 2 AF1988 fdxN element site-
983 32 34.8 515 2 T14340 sucrose-proton tra
984 32 34.8 518 2 AH3616 N-acylmannosamine
985 32 34.8 519 2 G84598 probable bZIP tran
986 32 34.8 523 2 C84753 hypothetical prote
987 32 34.8 524 2 A29600 alkaline phosphata
988 32 34.8 526 2 A41698 cell division cont
989 32 34.8 538 2 A83018 probable sodium/hy
990 32 34.8 551 2 AC2311 hypothetical prote
991 32 34.8 556 2 G88941 protein R13D1.8 [
992 32 34.8 559 2 C75286 hypothetical prote
993 32 34.8 561 2 S62552 hypothetical prote
994 32 34.8 562 2 T33174 hypothetical prote
995 32 34.8 565 2 T47330 hypothetical prote
996 32 34.8 565 2 A13356 comE operon protei
997 32 34.8 566 2 F97224 lon-like ATP-depen
998 32 34.8 569 2 T02435 probable oxyterol
999 32 34.8 570 2 T46261 hypothetical prote
1000 32 34.8 572 2 S44415 malate dehydrogena

ALIGNMENTS

RESULT 1
AMHUB
natriuretic peptide B precursor [validated] - human
N:Alternate names: brain natriuretic factor-32 (BNF-32); brain natriuretic protein precursor
N:Contains: brain alpha natriuretic peptide; brain gamma natriuretic factor
C:Species: Homo sapiens (man)
C>Date: 07-Sep-1990 #sequence revision 02-Dec-1994 #text_change 09-Jul-2004
R:Seilhauer, J.J.; Arfsten, A.; Miller, J.A.; Lundquist, P.; Scarborough, R.M.; Lewicki, Biochem. Biophys. Res. Commun. 159, 650-658, 1989
A:Title: Human and canine gene homologs of porcine brain natriuretic peptide.
A:Reference number: A36736; MUID:90088474; PMID:2597152
A:Accession: A36736
A:Molecule type: DNA
A:Residues: 1-134 <SD>
A:Cross-references: UNIPROT:P16860; UNIPARC:UPI00000350A5; GB:M31776; NID:gl79514; PIDN:R:Sudoh, T.; Maekawa, K.; Kojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H. Biochem. Biophys. Res. Commun. 159, 1427-1434, 1989
A:Title: Cloning and sequence analysis of cDNA encoding a precursor for human brain natriuretic peptide.
A:Reference number: A30163; MUID:89193743; PMID:2522777
A:Accession: A30163
A:Molecule type: mRNA
A:Residues: 1-134 <SD>
A:Cross-references: UNIPARC:UPI00000350A5; GB:M31776; NID:gl79514; PIDN:R:Kambayashi, Y.; Nakao, K.; Mukoyama, M.; Saito, Y.; Ogawa, Y.; Shiono, S.; Inouye, K.; FEBS Lett. 259, 341-345, 1990
A:Title: Isolation and sequence determination of human brain natriuretic peptide in human brain.
A:Reference number: A34143; MUID:90092577; PMID:2136732
A:Accession: A34143
A:Molecule type: protein
A:Residues: 103-134 <KAM>
A:Cross-references: UNIPARC:UPI00000350A8
R:Hino, J.; Tateyama, H.; Minamino, N.; Kangawa, K.; Matsuo, H. Biochem. Biophys. Res. Commun. 167, 693-700, 1990
A:Title: Isolation and identification of human brain natriuretic peptides in cardiac atria.
A:Reference number: A90161; MUID:90211249; PMID:2138890
A:Accession: A34661
A:Molecule type: protein
A:Residues: 27-58 <HIN>
A:Cross-references: UNIPARC:UPI00001733AB
A:Accession: B34661
A:Molecule type: protein
A:Residues: 103-134 <H12>
A:Cross-references: UNIPARC:UPI00001733AB
C:Genetics:
A:Gene: GDB:NPPB

A:Cross-references: GDB:L27884; OMIM:600295
A:Map position: lp36-lp36
A:Introns: 44/3; 130/1
C:Superfamily: natriuretic peptide A precursor
C:Keywords: brain; diuretic; hormone; natriuretic; osmoregulation
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-134/Product: brain gamma natriuretic factor #status experimental <GNF>
F:103-134/Product: brain alpha natriuretic peptide #status experimental <ANF>
F:112-128/Disulfide bonds: #status predicted

Query Match 100.0%; Score 92; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 9.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSGLGC 17
|||||
Db 112 CFGRKMDRISSSGLGC 128

RESULT 2
JC1081
brain natriuretic peptide - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 16-Feb-1997
C:Accession: JC1081
R:Chen, H.; Zhang, J.; Wang, Q.S.; Cui, H.; Tang, J. J. Fudan Univ. (Natur. Sci.) 30, 413-416, 1991
A:Title: Chemical synthesis and cloning of the porcine brain natriuretic gene.
A:Reference number: JC1081
A:Accession: JC1081
A:Molecule type: DNA
A:Residues: 1-27 <CHE>
A:Cross-references: UNIPARC:UPI0000176582
A>Note: The translation of the start codon ATG is not given in this paper
C:Genetics:
A:Gene: bnp
C:Superfamily: natriuretic peptide A precursor
C:Keywords: brain; natriuretic

Query Match 82.6%; Score 76; DB 2; Length 27;
Best Local Similarity 76.5%; Pred. No. 1.2e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSGLGC 17
|||||
Db 5 CFGRKMDRISSSGLGC 21

RESULT 3
A41403
aldosterone secretion inhibitory factor precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A41403; A30976
R:Nguyen, T.T.; Lazure, C.; Babinski, K.; Chretien, M.; De Lean, A.; Ong, H. Mol. Endocrinol. 3, 1823-1829, 1989
A:Title: Purification and primary structure of pro-aldosterone secretion inhibitory factor.
A:Reference number: A41403; MUID:90114187; PMID:2532709
A:Accession: A41403
A:Molecule type: protein
A:Residues: 1-103 <NGU>
A:Cross-references: UNIPROT:P13204; UNIPARC:UPI0000125AD9
R:Nguyen, T.T.; Lazure, C.; Babinski, K.; Chretien, M.; Ong, H.; de Lean, A. Endocrinology 124, 1591-1593, 1989
A:Title: Aldosterone secretion inhibitory factor: a novel neuropeptide in bovine chromaffin cells.
A:Reference number: A30976; MUID:89136947; PMID:2537187
A:Accession: A30976
A:Molecule type: protein
A:Residues: 69-103 <NG2>
A:Cross-references: UNIPARC:UPI0000176580
C:Superfamily: natriuretic peptide A precursor

Query Match 82.6%; Score 76; DB 2; Length 103;

Best Local Similarity 76.5%; Pred. No. 4.8e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
||||:|||||
Db 81 CFGRRLDRIIGLSGLGC 97

RESULT 4

A36736
brain natriuretic peptide - dog
C:Species: Canis lupus familiaris (dog)
C>Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Jul-2004
C:Accession: B36736
R;Seilhamer, J.J.; Arfsten, A.; Miller, J.A.; Lundquist, P.; Scarborough, R.M.; Lewicki, J. Biochem. Biophys. Res. Commun. 165, 650-658, 1989
A:Title: Human and canine gene homologs of porcine brain natriuretic peptide.
A:Reference number: A36736; MUID:90088474; PMID:2597152
A:Accession: B36736
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-105 <SEI>
A:Cross-references: UNIPROT:P16859; UNIPARC:UPI0000176581; GB:M31777
C:Superfamily: natriuretic peptide A precursor

Query Match 82.6%; Score 76; DB 2; Length 105;

Best Local Similarity 76.5%; Pred. No. 4.9e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
||||:|||||
Db 83 CFGRRLDRIIGLSGLGC 99

RESULT 5

A31676
brain natriuretic factor precursor - pig
N:Alternate names: brain natriuretic factor 32
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C:Accession: A31676; A31517; S06359
R;Maekawa, K.; Sudoh, T.; Furusawa, M.; Minamino, N.; Kangawa, K.; Ohkubo, H.; Nakanishi, Biochem. Biophys. Res. Commun. 157, 410-416, 1988
A:Title: Cloning and sequence analysis of cDNA encoding a precursor for porcine brain natriuretic factor.
A:Reference number: A31676; MUID:89061744; PMID:3196348
A:Accession: A31676
A:Molecule type: mRNA
A:Residues: 1-131 <NAE>
A:Cross-references: UNIPROT:P07634; UNIPARC:UPI00001561A8; GB:M23596; NID:G535704; PIDN:R;Sudoh, T.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 155, 726-732, 1988
A:Title: Brain natriuretic peptide-32: N-terminal six amino acid extended form of brain natriuretic factor.
A:Reference number: A31517; MUID:88339957; PMID:3421965
A:Accession: A31517
A:Molecule type: protein
A:Residues: 100-131 <SUD>
A:Cross-references: UNIPARC:UPI000003520D
R;Sudoh, T.; Kangawa, K.; Minamino, N.; Matsuo, H.
Nature 332, 78-81, 1988
A:Title: A new natriuretic peptide in porcine brain.
A:Reference number: S06359; MUID:88156915; PMID:2964562
A:Accession: S06359
A:Molecule type: protein
A:Residues: 106-131 <SU2>
A:Cross-references: UNIPARC:UPI000003520C
C:Superfamily: natriuretic peptide A precursor
C:Keywords: brain; natriuretic
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-131/Product: brain gamma natriuretic factor #status predicted <GAM>
F:100-131/Product: brain alpha natriuretic peptide #status experimental <ALF>
F:109-125/Disulfide bonds: #status experimental

Query Match 82.6%; Score 76; DB 2; Length 131;

Best Local Similarity 76.5%; Pred. No. 6.1e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
||||:|||||
Db 109 CFGRRLDRIIGLSGLGC 125

RESULT 6

A33873
brain natriuretic peptide precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
C:Accession: A33873; A31675
R;Porter, J.G.; Arfsten, A.; Palisi, T.; Scarborough, R.M.; Lewicki, J.A.; Seilhamer, J. J. Biol. Chem. 264, 6689-6692, 1989
A:Title: Cloning of a cDNA encoding porcine brain natriuretic peptide.
A:Reference number: A33873; MUID:89214071; PMID:2708334
A:Accession: A33873
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <POR>
A:Cross-references: UNIPROT:P07634; UNIPARC:UPI0000125ADB; GB:M25547; GB:J04708; GB:M22101
R;Minamino, N.; Kangawa, K.; Matsuo, H. Biochem. Biophys. Res. Commun. 157, 402-409, 1988
A:Title: Isolation and identification of a high molecular weight brain natriuretic peptide.
A:Reference number: A31675; MUID:89061743; PMID:3196347
A:Accession: A31675
A>Status: preliminary
A:Molecule type: protein
A:Residues: 26-131 <MIN>
A:Cross-references: UNIPARC:UPI000017657F
C:Superfamily: natriuretic peptide A precursor

Query Match 82.6%; Score 76; DB 2; Length 131;

Best Local Similarity 76.5%; Pred. No. 6.1e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
||||:|||||
Db 109 CFGRRLDRIIGLSGLGC 125

RESULT 7

S71381
lebetin 2 isoform alpha - Vipera lebetina
C:Species: Vipera lebetina
C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C:Accession: S71381; S71382; S71379
R;Barbouche, R.; Marrakchi, N.; Mansuette, P.; Krifi, M.; Fenouillet, E.; Rochat, H.; E. FEBS Lett. 392, 6-10, 1996
A:Title: Novel anti-platelet aggregation polypeptides from Vipera lebetina venom: isolation and characterization of two peptides.
A:Reference number: S71379; MUID:96354866; PMID:8769304
A:Accession: S71381
A:Molecule type: protein
A:Residues: 1-38 <BAR>
A:Cross-references: UNIPROT:Q7LZ09; UNIPARC:UPI0000030733
A:Experimental source: venom
A:Accession: S71382
A:Molecule type: protein
A:Residues: 2-38 <BA2>
A:Cross-references: UNIPARC:UPI0000030734
A:Experimental source: venom
A:Accession: S71379
A:Molecule type: protein
A:Residues: 1-13 <BA3>
A:Cross-references: UNIPARC:UPI000003072F
A:Experimental source: venom
C:Keywords: anticoagulant; venom
F:14-30/Disulfide bonds: #status predicted

Query Match 80.4%; Score 74; DB 2; Length 38;
Best Local Similarity 76.5%; Pred. No. 3.9e-06;

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Matches 13; Conservative 1; Mismatches 3; Indels 0; Gap# 0;

QY 1 CFGRKMDRISSSSGLGC 17
   ||| |:||| |:|||
Db 14 CFGHKIDRIGSHSGLGC 30

RESULT 8
A36155
natriuretic peptide C precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A36155; A35423; A34642
R:Tawaragi, Y.; Fuchimura, K.; Nakazato, H.; Tanaka, S.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 172, 627-632, 1990
A:Title: Gene and precursor structure of porcine C-type natriuretic peptide.
A:Reference number: A36155; MUID:91054475; PMID:2146957
A:Accession: A36155
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-126 <TAW>
A:Cross-references: UNIPARC:UPI0000125AE0; EMBL:M64758; NID:g309789; PID
R:Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 170, 973-979, 1990
A:Title: N-terminally extended form of C-type natriuretic peptide (CNP-53) identified in
A:Reference number: A35423; MUID:90343827; PMID:2383278
A:Accession: A35423
A:Status: preliminary
A:Molecule type: protein
A:Residues: 74-126 <MIN>
A:Cross-references: UNIPARC:UPI0000035212
R:Sudoh, T.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 168, 863-870, 1990
A:Title: C-type natriuretic peptide (CNP): a new member of natriuretic peptide family id
A:Reference number: A34642; MUID:90241265; PMID:2139780
A:Accession: A34642
A:Status: preliminary
A:Molecule type: protein
A:Residues: 105-126 <SUD>
A:Cross-references: UNIPARC:UPI0000033C90
C:Superfamily: natriuretic peptide C precursor
C:Keywords: disulfide bond; diuretic; hormone; natriuretic; osmoregulation
F:1-23/Domain: signal sequence #status predicted <SIG>
F:74-126/Product: natriuretic peptide C-53 #status experimental <C53>
F:98-126/Product: natriuretic peptide C-29 #status predicted <C29>
F:105-126/Product: natriuretic peptide C-22 #status experimental <C22>
F:110-126/Disulfide bonds: #status predicted

Query Match 79.3%; Score 73; DB 1; Length 126;
Best Local Similarity 76.5%; Pred. No. 2e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gap# 0;

QY 1 CFGRKMDRISSSSGLGC 17
   ||| |:||| |:|||
Db 110 CFGLKLDRIGSMGLGC 126

RESULT 9
AWHUC
natriuretic peptide C precursor [validated] - human
N:Alternate names: natriuretic factor C
N:Contents: natriuretic peptide C-22; natriuretic peptide C-29; natriuretic peptide C-53
C:Species: Homo sapiens (man)
C>Date: 17-Apr-1993 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C:Accession: JT0567; JCI361; I54400
R:Tawaragi, Y.; Fuchimura, K.; Tanaka, S.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 175, 645-651, 1991
A:Title: Gene and precursor structures of human C-type natriuretic peptide.
A:Reference number: JT0567; MUID:91207363; PMID:2018508
A:Accession: JT0567
A:Molecule type: DNA
A:Residues: 1-126 <TAW>
A:Cross-references: UNIPROT:P23582; UNIPARC:UPI0000033C91; GB:M64710; NID:g180676; PIDN:
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R:Ishizaka, Y.; Kangawa, K.; Minamino, N.; Ishii, K.; Takano, S.; Eto, T.; Matsuo, H.
Biochem. Biophys. Res. Commun. 189, 697-704, 1992
A:Title: Isolation and identification of C-type natriuretic peptide in human monocyte
A:Reference number: JCI361; MUID:93112033; PMID:1472040
A:Accession: JCI361
A:Molecule type: protein
A:Residues: 98-109, 'X', 111-118 <ISH>
A:Cross-references: UNIPARC:UPI00001733AE
R:Ogawa, Y.; Nakao, K.; Nakagawa, O.; Komatsu, Y.; Hosoda, K.; Suga, S.; Arai, H.; Nagat
Hypertension 19, 809-813, 1992
A:Title: Human C-type natriuretic peptide, Characterization of the gene and peptide.
A:Reference number: I54400; MUID:92275775; PMID:1339402
A:Accession: I54400
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-126 <RES>
A:Cross-references: UNIPARC:UPI0000033C91; GB:D90337; NID:g219542; PIDN:BAA14351.1; PID:
C:Genetics:
A:Gene: GDB:NPPC
A:Cross-references: GDB:250346; OMIM:600296
A:Map position: 2pter-2qter
C:Introns: 30/3
C:Superfamily: natriuretic peptide C precursor
C:Keywords: brain; diuretic; hormone; natriuretic; neuropeptide; osmoregulation
F:1-23/Domain: signal sequence #status predicted <SIG>
F:74-126/Product: natriuretic peptide C-53 #status predicted <C53>
F:98-126/Product: natriuretic peptide C-29 #status experimental <C29>
F:105-126/Product: natriuretic peptide C-22 #status predicted <C22>
F:110-126/Disulfide bonds: #status predicted

Query Match 79.3%; Score 73; DB 1; Length 126;
Best Local Similarity 76.5%; Pred. No. 2e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   ||| |:||| |:|||
Db 110 CFGLKLDRIGSMGLGC 126

RESULT 10
A55688
natriuretic peptide c precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C:Accession: A55688
R:Ogawa, Y.; Itoh, H.; Yoshitake, Y.; Inoue, M.; Yoshimasa, T.; Serikawa, T.; Nakao, K.
Genomics 24, 383-387, 1994
A:Title: Molecular cloning and chromosomal assignment of the mouse C-type natriuretic p
A:Reference number: A55688; MUID:95213034; PMID:7698765
A:Accession: A55688
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-126 <OGA>
A:Cross-references: UNIPROT:Q61839; UNIPARC:UPI0000003FF3; GB:D28873; NID:g633087; PIDN
C:Genetics:
A:Gene: Nppc
C:Superfamily: natriuretic peptide C precursor

Query Match 79.3%; Score 73; DB 2; Length 126;
Best Local Similarity 76.5%; Pred. No. 2e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   ||| |:||| |:|||
Db 110 CFGLKLDRIGSMGLGC 126

RESULT 11
S12988
brain natriuretic peptide type C - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S12988
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R.;Kojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.
FEBS Lett. 276, 209-213, 1990
A;Title: Cloning and sequence analysis of a cDNA encoding a precursor for rat C-type natriuretic peptide.
A;Reference number: S12988; MUID:91092420; PMID:1702395
A;Accession: S12988
A;Molecule type: mRNA
A;Residues: 1-126 <KOJ>
A;Cross-references: UNIPROT:P55207; UNIPARC:UPI0000125AE2; GB:D90219; NID:g220711; PIDN:
C;Superfamily: natriuretic peptide C precursor

Query Match 79.3%; Score 73; DB 2; Length 126;
Best Local Similarity 76.5%; Pred. No. 2e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
|||:|||||
DB 110 CFGLKLDRIKSMGLGC 126
|||:|||||

RESULT 12
S14320
alpha-atrial natriuretic peptide precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S14320; A31509
R;Akizuki, N.; Kangawa, K.; Minamino, N.; Matsuo, H.
FEBS Lett. 280, 357-362, 1991
A;Title: Cloning and sequence analysis of complementary DNA encoding a precursor for chicken atrial natriuretic peptide.
A;Reference number: S14320; MUID:91192169; PMID:1826483
A;Accession: S14320
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <AKI>
A;Cross-references: UNIPROT:P18908; UNIPARC:UPI0000125AFA; GB:X57702; NID:g63648; PIDN:
R;Miyata, A.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 155, 1330-1337, 1988
A;Title: Identification of a 29-amino acid natriuretic peptide in chicken heart.
A;Reference number: A31509; MUID:89025805; PMID:2972278
A;Accession: A31509
A;Molecule type: protein
A;Residues: 112-140 <MIY>
A;Cross-references: UNIPARC:UPI00000351EC
C;Superfamily: natriuretic peptide A precursor
F;118-134/Disulfide bonds: #status experimental

Query Match 79.3%; Score 73; DB 1; Length 140;
Best Local Similarity 70.6%; Pred. No. 2.2e-05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
|||:|||||
DB 118 CFGRIDRIKSLGMGC 134
|||:|||||

RESULT 13
JT0581
natriuretic peptide type C - chicken
C;Species: Gallus gallus (chicken)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JT0581
R;Arimura, J.J.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 174, 142-148, 1991
A;Title: Isolation and identification of C-type natriuretic peptide in chicken brain.
A;Reference number: JT0581; MUID:91113186; PMID:1989595
A;Accession: JT0581
A;Molecule type: protein
A;Residues: 1-22 <ARI>
A;Cross-references: UNIPROT:P21805; UNIPARC:UPI0000035211
A;Experimental source: brain
C;Superfamily: natriuretic peptide A precursor
C;Keywords: diuretic; hormone; natriuretic; osmoregulation

Query Match 78.3%; Score 72; DB 2; Length 22;
Best Local Similarity 76.5%; Pred. No. 6.2e-06;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Best Local Similarity 76.5%; Pred. No. 5e-06;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
|||:|||||
DB 6 CFGLKLDRIKSMGLGC 22
|||:|||||

RESULT 14
A35418
brain natriuretic peptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
C;Accession: A35418
R;Takei, Y.; Takahashi, A.; Watanabe, T.X.; Nakajima, K.; Sakakibara, S.; Takao, T.; Sh
Biochem. Biophys. Res. Commun. 170, 883-891, 1990
A;Title: Amino acid sequence and relative biological activity of a natriuretic peptide
A;Reference number: A35418; MUID:90343814; PMID:2143379
A;Accession: A35418
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <TAK>
A;Cross-references: UNIPROT:P18145; UNIPARC:UPI000003520A
C;Superfamily: natriuretic peptide A precursor

Query Match 78.3%; Score 72; DB 2; Length 22;
Best Local Similarity 76.5%; Pred. No. 5e-06;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
|||:|||||
DB 6 CFGLKLDRIKSLGLGC 22
|||:|||||

RESULT 15
A33431
atrial natriuretic factor - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
C;Accession: A33431
R;Takei, Y.; Takahashi, A.; Watanabe, T.X.; Nakajima, K.; Sakakibara, S.
Biochem. Biophys. Res. Commun. 164, 537-543, 1989
A;Title: Amino acid sequence and relative biological activity of eel atrial natriuretic
A;Reference number: A33431; MUID:90026430; PMID:2529857
A;Accession: A33431
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-27 <TAK>
A;Cross-references: UNIPROT:P18144; UNIPARC:UPI00000351F9
C;Superfamily: natriuretic peptide A precursor

Query Match 78.3%; Score 72; DB 2; Length 27;
Best Local Similarity 76.5%; Pred. No. 6.2e-06;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
|||:|||||
DB 7 CFGLKLDRIKSYSLGC 23
|||:|||||

RESULT 16
S15821
ventricular natriuretic peptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: S15821
R;Takei, Y.; Takahashi, A.; Watanabe, T.X.; Nakajima, K.; Sakakibara, S.
FEBS Lett. 282, 317-320, 1991
A;Title: A novel natriuretic peptide isolated from eel cardiac ventricles.
A;Reference number: S15821; MUID:91243821; PMID:1828035
A;Accession: S15821
A;Molecule type: protein
A;Residues: 1-36 <FEB>

Proc. Natl. Acad. Sci. U.S.A. 81, 6325-6329, 1984
A:Title: Molecular cloning and characterization of DNA sequences encoding rat and human
A:Reference number: I39458; MUID:85038509; PMID:6238331
A:Accession: I39458
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 119-151, 'RR' <RE2>
A:Cross-references: UNIPARC:UPI000002DD32; GB:X02044; NID:g178631; PIDN:AAA51730.1; PID:
R;Waki, M.; Parmentier, M.; Inagami, T.
Biochem. Biophys. Res. Commun. 125, 797-802, 1984
A:Title: Cloning of genomic DNA for human atrial natriuretic factor.
A:Reference number: I39459; MUID:85096983; PMID:6097248
A:Accession: I39459
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-75 <RE3>
A:Cross-references: UNIPARC:UPI000016A556; GB:X02399; NID:g178633; PIDN:AAA35528.1; PID:
R;Seidman, C.E.; Bloch, K.D.; Zisfein, J.; Smit, J.; Haber, E.; Homcy, C.J.; Duby, A.D.;
Hypertension 7, 31-34, 1985
A:Title: Molecular studies of the atrial natriuretic factor gene.
A:Reference number: I39460
A:Accession: I39460
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-64, 'D', '66-151' <RE4>
A:Cross-references: UNIPARC:UPI000016A557; GB:M54951; NID:g178636; PIDN:AAA35529.1; PID:
R;Greenberg, B.D.; Bencen, G.H.; Seilhamer, J.J.; Lewicki, J.A.; Fiddes, J.C.
Nature 312, 656-658, 1984
A:Title: Nucleotide sequence of the gene encoding human atrial natriuretic factor precursor
A:Reference number: I37167; MUID:85061627; PMID:6095119
A:Accession: I37167
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 26-151 <RE5>
A:Cross-references: UNIPARC:UPI0000156DAE; EMBL:X01471; NID:g28690; PIDN:CAA25700.1; PID:
C;Comment: Cardiolipin is a vasoconstrictor but not a diuretic or natriuretic.
C;Genetics:
A:Gene: GDB:NPPA; ANP; PND
A:Cross-references: GDB:118727; OMIM:108780
A:Map position: 1p36-1p36
A:Introns: 41/3; 150/3
C:Superfamily: natriuretic peptide A precursor
C:Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-151/Product: cardiolipin #status predicted <COD>
F:124-151/Product: atrial alpha natriuretic peptide #status experimental <ANP>
F:130-146/Disulfide bonds: #status experimental

Query Match 77.2%; Score 71; DB 1; Length 151;
Best Local Similarity 70.6%; Pred. No. 5.4e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 130 CFGGRMDRIGASGLGC 146

RESULT 20
ANBO
A:Title: natriuretic peptide precursor - bovine
A:Alternate names: ANP; atrial natriuretic polypeptide
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A90124; A93049; A24247; A26090
R;Vlasuk, G.P.; Miller, J.; Bencen, G.H.; Lewicki, J.A.
Biochem. Biophys. Res. Commun. 136, 396-403, 1986
A:Title: Structure and analysis of the bovine atrial natriuretic peptide precursor gene.
A:Reference number: A90124; MUID:86215205; PMID:2939830
A:Accession: A90124
A:Molecule type: DNA
A:Residues: 1-152 <VIA>
A:Cross-references: UNIPROT:P07501; UNIPARC:UPI0000125AF7; GB:M13145; NID:g162665; PIDN:
R;Ong, H.; McNicoll, N.; Lazure, C.; Seidah, N.; Chretien, M.; Cantin, M.; De Lean, A.

Life Sci. 38, 1309-1315, 1986
A:Title: Purification and sequence determination of bovine atrial natriuretic factor.
A:Reference number: A93049; MUID:86173941; PMID:3007908
A:Accession: A93049
A:Molecule type: protein
A:Residues: 123-150 <ONG>
A:Cross-references: UNIPARC:UPI000002B7D3
C;Genetics:
A:Introns: 40/3; 149/3
C:Superfamily: natriuretic peptide A precursor
C:Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-152/Product: gamma atrial natriuretic factor #status predicted <ANP>
F:123-150/Product: alpha atrial natriuretic peptide #status experimental <ANP>
F:129-145/Disulfide bonds: #status predicted

Query Match 77.2%; Score 71; DB 1; Length 152;
Best Local Similarity 70.6%; Pred. No. 5.4e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 129 CFGGRMDRIGASGLGC 145

RESULT 21
SI4873
A:Title: natriuretic peptide precursor - horse
C:Species: Equus caballus (domestic horse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: SI4873
R;Maegert, H.J.; Hanke, M.; Schmedding, G.; Teuteberg, K.; Schulz-Knappe, P.; Forssmann,
submitted to the EMBL Data Library, March 1991
A:Reference number: SI4872
A:Accession: SI4873
A:Molecule type: mRNA
A>Status: preliminary
A:Residues: 1-153 <MAE>
A:Cross-references: UNIPROT:P27104; UNIPARC:UPI0000125AFB; EMBL:X58563; NID:g1008; PIDN:
C:Superfamily: natriuretic peptide A precursor

Query Match 77.2%; Score 71; DB 2; Length 153;
Best Local Similarity 70.6%; Pred. No. 5.8e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
DB 130 CFGGRMDRIGASGLGC 146

RESULT 22
IS5480
A:Title: hypothetical natriuretic peptide/phage fr coat protein mutant fusion protein - synthetic
C:Species: synthetic
A:Date: Homo sapiens (man) and phage fr genes engineered and expressed in Escherichia coli
C:Date: 02-Jul-1996 #sequence_revision 05-Sep-1996 #text_change 20-Oct-2000
C:Accession: IS5480
R;Berzins, V.; Jansone, I.; Skangals, A.; Kalnins, P.; Liepa, S.; Baumanis, V.
J. Biotechnol. 30, 231-243, 1993
A:Title: High level expression of alpha-human atrial natriuretic factor as a fusion pol.
A:Reference number: IS5480; MUID:93384792; PMID:7764035
A:Accession: IS5480
A:Molecule type: DNA
A:Residues: 1-161 <BER>
A:Cross-references: UNIPARC:UPI0000045710; GB:S66567; NID:g435742; PIDN:AAC60713.1; PID:
C:Keywords: fusion protein

Query Match 77.2%; Score 71; DB 4; Length 161;
Best Local Similarity 70.6%; Pred. No. 5.8e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17

Db 140 CFGKMDRIGASGLGC 156
||||:||||:|||||
RESULT 23
B54119
C-type natriuretic peptide II precursor - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: B54119
R:Kojima, M.; Ohyama, Y.; Miyamoto, K.; Minamino, N.; Kangawa, K.; Matsuo, H.
J. Biol. Chem. 269, 13136-13140, 1994
A:Title: Cloning and characterization of a novel natriuretic peptide in frog (Rana catesbeiana)
A:Reference number: A54119; MUID:94230409; PMID:8175740
A:Accession: B54119
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <KOJ>
A:Cross-references: UNIPROT:P40756; UNIPARC:UPI0000125AE5; GB:D17414; NID:G397835; PIDN:G397835
A:Note: authors translated the codon AAA for residue 89 as Ile
C:Superfamily: natriuretic peptide C precursor
Query Match 76.1%; Score 70; DB 2; Length 118;
Best Local Similarity 70.6%; Pred. No. 6.3e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGKMDRIGASGLGC 17
||||:||||:|||||
Db 102 CFGKMDRIGASGLGC 118
RESULT 24
A61244
natriuretic peptide type C precursor - spiny dogfish
C:Species: Squalus acanthias (spiny dogfish)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A61244; 151329
R:Schofield, J.P.; Jones, D.S.C.; Forrest Jr., J.N.
Am. J. Physiol. 261, F734-F739, 1991
A:Title: Identification of C-type natriuretic peptide in heart of spiny dogfish shark (Sphyrna tiburo)
A:Reference number: A61244; MUID:92026459; PMID:1928383
A:Accession: A61244
A:Molecule type: mRNA
A:Residues: 1-135 <SCH>
A:Cross-references: UNIPROT:P41319; UNIPARC:UPI0000125AE5; EMBL:X59991; NID:G556803; PIDN:G556803
C:Genetics:
A:Introns: 30/3
C:Superfamily: natriuretic peptide A precursor
C:Keywords: disulfide bond; diuretic; hormone; natriuretic; osmoregulation
F;1-25/Domain: signal sequence #status predicted <SIG>
F;114-135/Product: natriuretic peptide C #status predicted <NPC>
F;119-135/Disulfide bonds: #status predicted
Query Match 76.1%; Score 70; DB 1; Length 135;
Best Local Similarity 70.6%; Pred. No. 7.3e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGKMDRIGASGLGC 17
||||:||||:|||||
Db 119 CFGKMDRIGASGLGC 135
RESULT 25
S15822
natriuretic peptide type C - smaller spotted catshark
C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S15822
R:Suzuki, R.; Takahashi, A.; Hazon, N.; Takei, Y.
FEBS Lett. 282, 321-325, 1991
A:Title: Isolation of high-molecular-weight C-type natriuretic peptide from the heart of the smaller spotted catshark (Scyliorhinus canicula)
A:Reference number: S15822; MUID:91243822; PMID:1828036
A:Accession: S15822

A:Molecule type: protein
A:Residues: 1-115 <FEB>
A:Cross-references: UNIPROT:P23259; UNIPARC:UPI0000125AE3
C:Superfamily: natriuretic peptide A precursor
Query Match 75.0%; Score 69; DB 1; Length 115;
Best Local Similarity 70.6%; Pred. No. 9.3e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGKMDRIGASGLGC 17
||||:||||:|||||
Db 99 CFGKMDRIGASGLGC 115
RESULT 26
A36399
C-type natriuretic peptide - frog
C:Species: Rana gen. sp. (frog)
C>Date: 01-Feb-1991 #sequence_revision 01-Feb-1991 #text_change 09-Jul-2004
C:Accession: A36399
R:Yoshihara, A.; Kozawa, H.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 173, 591-598, 1990
A:Title: Isolation and sequence determination of frog C-type natriuretic peptide.
A:Reference number: A36399; MUID:91083642; PMID:2148082
A:Accession: A36399
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-22 <YOS>
A:Cross-references: UNIPROT:P20968; UNIPARC:UPI00001566AB
C:Superfamily: natriuretic peptide A precursor
Query Match 73.9%; Score 68; DB 2; Length 22;
Best Local Similarity 70.6%; Pred. No. 2.6e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGKMDRIGASGLGC 17
||||:||||:|||||
Db 6 CFGKMDRIGASGLGC 22
RESULT 27
A54119
c-type natriuretic peptide I precursor - bullfrog
N:Alternate names: CNP I
C:Species: Rana catesbeiana (bullfrog)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A54119
R:Kojima, M.; Ohyama, Y.; Miyamoto, K.; Minamino, N.; Kangawa, K.; Matsuo, H.
J. Biol. Chem. 269, 13136-13140, 1994
A:Title: Cloning and characterization of a novel natriuretic peptide in frog (Rana catesbeiana)
A:Reference number: A54119; MUID:94230409; PMID:8175740
A:Accession: A54119
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <KOJ>
A:Cross-references: UNIPROT:P20968; UNIPARC:UPI0000125AE1; GB:D17413; NID:G397837; PIDN:G397837
C:Superfamily: natriuretic peptide A precursor
Query Match 73.9%; Score 68; DB 1; Length 129;
Best Local Similarity 70.6%; Pred. No. 0.00016;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGKMDRIGASGLGC 17
||||:||||:|||||
Db 113 CFGKMDRIGASGLGC 129
RESULT 28
A29370
atrial natriuretic peptide precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
A:Accession: A29370; B43619

R;Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.; Seidman, J.G.
 Science 226, 1206-1209, 1984
 A;Title: Nucleotide sequences of the human and mouse atrial natriuretic factor genes.
 A;Reference number: A29370; MUID:85065766; PMID:6542248
 A;Accession: A29370
 A;Molecule type: DNA
 A;Residues: 1-152 <SEI>
 A;Cross-references: UNIPROT:P05125; UNIPARC:UPI0000027BFB; GB:K02781; NID:g191937; PIDN:
 C;Genetics:
 A;Introns: 40/3; 149/3
 C;Superfamily: natriuretic peptide A precursor
 C;Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-150/Product: gamma atrial natriuretic factor #status predicted <ANP>
 F;123-150/Product: alpha atrial natriuretic peptide #status predicted <ANP>
 F;129-145/Disulfide bonds: #status predicted

Query Match 72.8%; Score 67; DB 1; Length 152;
 Best Local Similarity 64.7%; Pred. No. 0.00028;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSGLGC 17
 ||| :||| :|||
 Db 129 CFGRIDRIGASGLGC 145

RESULT 29
 ANRT
 atrial natriuretic factor precursor - rat
 N;Contains: ANF(1-33); ANF(2-33); ANF(3-33); ANF(8-33); atrial natriuretic peptide; atr
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 19-Feb-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
 A;Accession: A22570; A01425; A93330; A43617; A93330; A94275; PT0061; A20973; A44190; A60
 R;Argentin, S.; Nemer, M.; Drouin, J.; Scott, G.K.; Kennedy, B.P.; Davies, P.L.
 J. Biol. Chem. 260, 4568-4571, 1985
 A;Title: The gene for rat atrial natriuretic factor.
 A;Reference number: A22570; MUID:85182558; PMID:2985557
 A;Accession: A22570
 A;Molecule type: DNA
 A;Residues: 1-152 <ARG>
 A;Cross-references: UNIPROT:P01161; UNIPARC:UPI0000125B00; GB:K02062; NID:g202899; PIDN:
 R;Yamanaka, M.; Greenberg, B.; Johnson, L.; Seilhamer, J.; Brewer, M.; Friedemann, T.; M
 Nature 309, 719-722, 1984
 A;Title: Cloning and sequence analysis of the cDNA for the rat atrial natriuretic factor
 A;Reference number: A93331; MUID:84219797; PMID:6547210
 A;Accession: A01425
 A;Molecule type: mRNA
 A;Residues: 1-152 <YAM>
 A;Cross-references: UNIPARC:UPI0000125B00; EMBL:X00665; NID:g55711; PIDN:CAA25285.1; PID
 R;Maki, M.; Takayanagi, R.; Misono, K.S.; Pandey, K.N.; Tibbetts, C.; Inagami, T.
 Nature 309, 722-724, 1984
 A;Title: Structure of rat atrial natriuretic factor precursor deduced from cDNA sequence
 A;Reference number: A93332; MUID:84219798; PMID:6328328
 A;Accession: A93332
 A;Molecule type: mRNA
 A;Residues: 1-152 <WAK>
 A;Cross-references: UNIPARC:UPI0000125B00; GB:X00665; EMBL:X00658; NID:g55711; PIDN:CAA2
 R;Seidman, C.E.; Duby, A.D.; Choi, E.; Graham, R.M.; Haber, E.; Homcy, C.; Smith, J.A.;
 Science 225, 324-325, 1984
 A;Title: The structure of rat preproatrial natriuretic factor as defined by a complement
 A;Reference number: A43617; MUID:84250178; PMID:6234658
 A;Accession: A43617
 A;Molecule type: mRNA
 A;Residues: 1-152 <SEI>
 A;Cross-references: UNIPARC:UPI0000125B00; GB:K02062; NID:g202899; PIDN:AAA40
 R;Atlas, S.A.; Kleiner, H.D.; Camargo, M.J.; Januszewicz, A.; Sealey, J.E.; Laragh, J.H
 Nature 309, 717-719, 1984
 A;Title: Purification, sequencing and synthesis of natriuretic and vasoactive rat atrial
 A;Reference number: A93330; MUID:84219796; PMID:6233494
 A;Accession: A93330
 A;Molecule type: protein
 A;Residues: 126-149 <ATL>
 A;Cross-references: UNIPARC:UPI00000351FC

R;Currie, M.G.; Geller, D.M.; Cole, B.R.; Siegel, N.R.; Fok, K.F.; Adams, S.P.; Eubanks
 Science 223, 67-69, 1984
 A;Title: Purification and sequence analysis of bioactive atrial peptides (atriopeptins)
 A;Reference number: A94275; MUID:84097513; PMID:6419347
 A;Accession: A94275
 A;Molecule type: protein
 A;Residues: 127-149 <CUR>
 A;Cross-references: UNIPARC:UPI00000351FB
 R;Thibault, G.; Murthy, K.K.; Gutkowska, J.; Seidah, N.G.; Lazure, C.; Chretien, M.; Ca
 Peptides 9, 47-53, 1988
 A;Title: NH2-terminal fragment of rat pro-atrial natriuretic factor in the circulation:
 A;Reference number: PT0061; MUID:88203350; PMID:2966345
 A;Accession: PT0061
 A;Molecule type: protein
 A;Residues: 25-28,'X',30-31,'X',33,'X',35-38 <THI>
 A;Cross-references: UNIPARC:UPI00001733AA
 R;Seidah, N.G.; Lazure, C.; Chretien, M.; Thibault, G.; Garcia, R.; Cantin, M.; Genest,
 Proc. Natl. Acad. Sci. U.S.A. 81, 2640-2644, 1984
 A;Title: Amino acid sequence of homologous rat atrial peptides: natriuretic activity of
 A;Reference number: A20973; MUID:84194062; PMID:6232612
 A;Accession: A20973
 A;Molecule type: protein
 A;Residues: 118-150 <SE2>
 A;Cross-references: UNIPARC:UPI000002BE79
 R;Flynn, T.G.; Davies, P.L.; Kennedy, B.P.; de Bold, M.L.; de Bold, A.J.
 Science 228, 323-325, 1985
 A;Title: Alignment of rat cardionatrin sequences with the preprocardionatrin sequence f
 A;Reference number: A44190; MUID:85168263; PMID:3157217
 A;Accession: A44190
 A;Molecule type: mRNA
 A;Residues: 1-152 <PLY>
 A;Cross-references: UNIPARC:UPI0000125B00; GB:K02062; NID:g202899; PIDN:AAA40735.1; PID
 A;Note: part of this sequence, including the amino ends of three mature peptides, was c
 R;Belcourt, D.; Vama, D.R.; Toney, K.; Bennett, H.P.J.
 Protein Expr. Purif. 1, 28-32, 1990
 A;Title: Purification of rat pro-atrial natriuretic factor: a simplified scheme using r
 A;Reference number: A60390; MUID:93044510; PMID:2152180
 A;Accession: A60390
 A;Molecule type: protein
 A;Residues: 25-39 <BEL>
 A;Cross-references: UNIPARC:UPI00000E66C9
 R;Gardner, D.G.; Vlasuk, G.P.; Baxter, J.D.; Fiddes, J.C.; Lewicki, J.A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 2175-2179, 1987
 A;Title: Identification of atrial natriuretic factor gene transcripts in the central ne
 A;Reference number: I59094; MUID:87175636; PMID:2951736
 A;Accession: I59094
 A;Status: translated from GB/EMBL/DBDJ
 A;Molecule type: mRNA
 A;Residues: 38-152 <RES>
 A;Cross-references: UNIPARC:UPI0000170882; GB:M15868; NID:g202903; PIDN:AAA40736.1; PID
 R;Kangawa, K.; Tawaragi, Y.; Oikawa, S.; Mizuno, A.; Sakuragawa, Y.; Nakazato, H.; Fuku
 Nature 312, 152-155, 1984
 A;Title: Identification of rat gamma atrial natriuretic polypeptide and characterizatio
 A;Reference number: I59057; MUID:85061500; PMID:6239103
 A;Accession: I59057
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: mRNA
 A;Residues: 1-152 <RE2>
 A;Cross-references: UNIPARC:UPI0000125B00; EMBL:X01118; NID:g55716; PIDN:CAA25586.1; PI
 R;Flynn, T.G.
 Can. J. Physiol. Pharmacol. 65, 2013-2020, 1987
 A;Title: The elucidation of the structure of atrial natriuretic factor, a new peptide h
 A;Reference number: I52678; MUID:88109092; PMID:2962707
 A;Accession: I52678
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: mRNA
 A;Residues: 1-51,'X',53-85,'X',87-152 <RE3>
 A;Cross-references: UNIPARC:UPI0000170883; GB:M27498; NID:g202905; PIDN:AAA40737.1; PID
 C;Comment: A disulfide bond is required for full activity of atriopetins.
 C;Genetics:
 A;Gene: ANF
 A;Introns: 40/3; 149/3

C;Superfamily: natriuretic peptide A precursor
C;Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-152/Product: pro-atrial natriuretic factor #status experimental <PRO>
F;25-150/Product: cardionatriin IV #status experimental <CN4>
F;773-150/Product: cardionatriin III #status experimental <CN3>
F;118-150/Product: ANF(1-33) #status experimental <ANF1>
F;119-150/Product: ANF(2-33) #status experimental <ANF2>
F;120-150/Product: ANF(3-33) #status experimental <ANF3>
F;123-150/Product: cardionatriin I #status experimental <CN1>
F;125-150/Product: ANF(8-33) #status experimental <ANF4>
F;126-150/Product: auriculin B #status experimental <AUB>
F;126-149/Product: auriculin A #status experimental <AUA>
F;127-150/Product: atrial natriuretic factor #status predicted <MAT>
F;127-149/Product: atriopeptin II #status experimental <AT1>
F;127-147/Product: atriopeptin I #status experimental <AT2>
F;129-145/Disulfide bonds: #status experimental

Query Match 72.8%; Score 67; DB 1; Length 152;
Best Local Similarity 64.7%; Pred. No. 0.00028;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGCG 17
DB 129 CFGGRIDRIGAQSGGCG 145

RESULT 30
ANRB
atrial natriuretic peptide precursor - rabbit
N;Alternate names: ANP; atrial natriuretic polypeptide
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: B25302
R;Okawa, S.; Inai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato, H.; Matsuo, H.
Biochem. Biophys. Res. Commun. 132, 892-899, 1985
A;Title: Structure of dog and rabbit precursors of atrial natriuretic polypeptides deduced from complementary DNA
A;Reference number: A90119; MUID:86076957; PMID:2934062
A;Molecule type: mRNA
A;Residues: 1-153 <OIK>
A;Cross-references: UNIPROT:P07500; UNIPARC:UPI0000125AF6; GB:M12046; NID:g164770; PIDN:
C;Superfamily: natriuretic peptide A precursor
C;Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-151/Product: gamma atrial natriuretic factor #status predicted <ANF>
F;124-151/Product: alpha atrial natriuretic peptide #status predicted <ANP>
F;130-146/Disulfide bonds: #status predicted

Query Match 72.8%; Score 67; DB 1; Length 153;
Best Local Similarity 64.7%; Pred. No. 0.00028;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGCG 17
DB 130 CFGGRIDRIGAQSGGCG 146

RESULT 31
S01657
atrial natriuretic factor - laughing frog (tentative sequence) (fragment)
N;Alternate names: atriopeptin
C;Species: Rana ridibunda (laughing frog)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S01657; A30977
R;Lazure, C.; Ong, H.; McNicoll, N.; Netchitailo, P.; Chretien, M.; de Lean, A.; Vaudry, R.
FEBS Lett. 238, 300-306, 1988
A;Title: The amino acid sequences of frog heart atrial natriuretic-like peptide and mammalian atrial natriuretic peptide
A;Reference number: S01657; MUID:89005705; PMID:2971573
A;Accession: S01657
A;Molecule type: protein
A;Residues: 1-30 <LAZ>
A;Cross-references: UNIPROT:P09196; UNIPARC:UPI00000351F2

A;Note: the sequence from the summary is inconsistent with that from Fig. 3 in lacking 1
C;Superfamily: natriuretic peptide A precursor

Query Match 71.7%; Score 66; DB 2; Length 30;
Best Local Similarity 58.8%; Pred. No. 8e-05;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGCG 17
DB 11 CFGSRIDRIGAQSGMGC 27

RESULT 32
JQ0947
atrial natriuretic peptide precursor - bullfrog
N;Alternate names: ANP; atrial natriuretic factor (ANF)
N;Contents: atrial natriuretic peptide-21; atrial natriuretic peptide-24
C;Species: Rana catesbeiana (bullfrog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JQ0947; A31510
R;Kojima, M.
submitted to JIPID, May 1991
A;Reference number: JQ0947
A;Accession: JQ0947
A;Molecule type: mRNA
A;Residues: 1-145 <KOJ>
A;Cross-references: UNIPROT:P18909; UNIPARC:UPI0000125AFF
R;Sakata, J.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 155, 1338-1345, 1988
A;Title: Identification of new atrial natriuretic peptides in frog heart.
A;Reference number: A31510; MUID:89025806; PMID:2972279
A;Accession: A31510
A;Molecule type: protein
A;Residues: 122-145 <SAK>
A;Cross-references: UNIPARC:UPI00000351EF
C;Comment: In mammals, several active peptides may be derived from the prohormone.
C;Superfamily: natriuretic peptide A precursor
C;Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-121/Domain: propeptide #status predicted <PRO>
F;122-145/Product: atrial natriuretic peptide-24 #status experimental <M24>
F;125-145/Product: atrial natriuretic peptide-21 #status experimental <M21>
F;125-141/Disulfide bonds: #status predicted

Query Match 71.7%; Score 66; DB 1; Length 145;
Best Local Similarity 58.8%; Pred. No. 0.0004;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLGCG 17
DB 125 CFGSRIDRIGAQSGMGC 141

RESULT 33
A49144
type-B natriuretic peptide, BNP - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A49144
R;Steinhilber, M.E.
Circ. Res. 72, 984-992, 1993
A;Title: Structure, expression, and genomic mapping of the mouse natriuretic peptide ty
A;Reference number: A49144; MUID:93238395; PMID:8097440
A;Accession: A49144
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-121 <STE>
A;Cross-references: UNIPARC:UPI0000176583; GB:S58667; NID:g299794; PIDN:AA26344.1; PID
A;Experimental source: BAB/c
A;Note: sequence inconsistent with the nucleotide translation
C;Superfamily: natriuretic peptide A precursor

```
Query Match          70.7%; Score 65; DB 2; Length 121;
Best Local Similarity 70.6%; Pred. No. 0.0005;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFGKMDRISSSSLG 17
    ||| : ||| : |||
Db 99 CFGHKIDRIGSVSL 115

RESULT 34
149548
brain natriuretic peptide - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49548
R;Ogawa, Y.; Itoh, H.; Tamura, N.; Suga, S.; Yoshimasa, T.; Uehira, M.; Matsuda, S.; Shi
J. Clin. Invest. 93, 1911-1921, 1994
A;Title: Molecular cloning of the complementary DNA and gene that encode mouse brain nat
A;Reference number: I49548; MUID:94237953; PMID:8182124
A;Accession: I49548
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-121 <RES>
A;Cross-references: UNIPROT:P40753; UNIPARC:UPI0000000CE3; GB:D16497; NID:g493659; PIDN:
C;Genetics:
A;Gene: BNP
A;Introns: 42/3; 117/1
C;Superfamily: natriuretic peptide A precursor

Query Match          70.7%; Score 65; DB 2; Length 121;
Best Local Similarity 70.6%; Pred. No. 0.0005;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFGKMDRISSSSLG 17
    ||| : ||| : |||
Db 99 CFGHKIDRIGSVSL 115

RESULT 35
S14872
atrial natriuretic peptide precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C:Accession: S14872
R;Maegert, H.J.; Hanke, M.; Schmieding, G.; Teuteberg, K.; Schulz-Knappe, P.; Forssmann,
submitted to the EMBL Data Library, March 1991
A;Reference number: S14872
A;Accession: S14872
A;Molecule type: mRNA
A;Residues: 1-128 <MAE>
A;Cross-references: UNIPROT:P27596; UNIPARC:UPI0000125AF9; EMBL:X58562; NID:g49543; PIDN:
A;Experimental source: heart atria; adult
C;Superfamily: natriuretic peptide A precursor
C;Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F;1-98/Domain: signal sequence #status predicted <SIG>
F;99-128/Product: atrial natriuretic peptide #status predicted <MAT>
F;105-121/Disulfide bonds: #status predicted

Query Match          70.7%; Score 65; DB 2; Length 128;
Best Local Similarity 64.7%; Pred. No. 0.00053;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFGKMDRISSSSLG 17
    ||| : ||| : |||
Db 105 CFGGRMDRIGAQSS 121

RESULT 36
A42974
natriuretic peptide, DNP - eastern green mamba
C:Species: Dendroaspis angusticeps (eastern green mamba)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42974
```

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R;Schweitz, H.; Vigne, P.; Moinier, D.; Frelin, C.; Lazdunski, M.
J. Biol. Chem. 267, 13928-13932, 1992
A;Title: A new member of the natriuretic peptide family is present in the venom of the
A;Reference number: A42974; MUID:92332489; PMID:1352773
A;Accession: A42974
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-38 <SCH>
A;Cross-references: UNIPROT:P28374; UNIPARC:UPI00000350A9
A;Note: sequence extracted from NCBI backbone (NCBIP:108360)
C;Superfamily: natriuretic peptide A precursor

Query Match          68.5%; Score 63; DB 2; Length 38;
Best Local Similarity 64.7%; Pred. No. 0.00035;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CFGKMDRISSSSLG 17
    ||| : ||| : |||
Db 7 CFGHKIDRINHVSNLG 23

RESULT 37
A30162
brain natriuretic factor precursor - rat
N;Alternate names: brain natriuretic peptide; cardiac natriuretic factor; iso-atrial na
N;Contains: brain natriuretic factor BNP-45
C;Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A30162; A35691; A54893; A32918; A33253; A60735; I57704; A33252
R;Kojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 159, 1420-1426, 1989
A;Title: Cloning and sequence analysis of cDNA encoding a precursor for rat brain natri
A;Reference number: A30162; MUID:89193742; PMID:2522776
A;Accession: A30162
A;Molecule type: mRNA
A;Residues: 1-121 <KOJ>
A;Cross-references: UNIPROT:P13205; UNIPARC:UPI0000125ADC; GB:M25297; NID:g602483; PIDN:
R;Roy, R.N.; Flynn, T.G.
Biochem. Biophys. Res. Commun. 171, 416-423, 1990
A;Title: Organization of the gene for iso-RANP, a rat B-type natriuretic peptide.
A;Reference number: A35691; MUID:90365739; PMID:2144113
A;Accession: A35691
A;Molecule type: DNA
A;Residues: 1-14,'V',16-121 <ROY>
A;Cross-references: UNIPARC:UPI00001709D6; GB:M60731; NID:g204985; PIDN:AAA41456.1; PID
A;Note: the authors translated the codon GGT for residue 15 as Leu
R;Thuerauf, D.J.; Hanford, D.S.; Glembofski, C.C.
J. Biol. Chem. 269, 17772-17775, 1994
A;Title: Regulation of rat brain natriuretic peptide transcription. A potential role fo
A;Reference number: A54893; MUID:94299479; PMID:8027030
A;Accession: A54893
A;Molecule type: DNA
A;Residues: 1-19 <THU>
A;Cross-references: UNIPARC:UPI0000000516; GB:U02972; NID:g458021; PIDN:AAA21648.1; PID
R;Aburaya, M.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 163, 226-232, 1989
A;Title: Isolation and identification of rat brain natriuretic peptides in cardiac atri
A;Reference number: A32918; MUID:89374230; PMID:2673236
A;Accession: A32918
A;Molecule type: protein
A;Residues: 27-121 <ABU>
A;Cross-references: UNIPARC:UPI00001733AC
R;Kambayashi, Y.; Nakao, K.; Itoh, H.; Hosoda, K.; Saito, Y.; Yamada, T.; Mukoyama, M.;
Imura, H.
Biochem. Biophys. Res. Commun. 163, 233-240, 1989
A;Title: Isolation and sequence determination of rat cardiac natriuretic peptide.
A;Reference number: A32919; MUID:89374231; PMID:2528349
A;Accession: A32919
A;Molecule type: protein
A;Residues: 77-121 <KAM>
A;Cross-references: UNIPARC:UPI000003520F
R;Flynn, T.G.; Brar, A.; Tremblay, L.; Sarda, I.; Lyons, C.; Jennings, D.B.
Biochem. Biophys. Res. Commun. 161, 830-837, 1989
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A>Title: Isolation and characterization of iso-rAMP, a new natriuretic peptide from rat
A:Reference number: A3253; MUID:89286593; PMID:2525380
A:Accession: A3253
A:Molecule type: protein
A:Residues: 77-119,'Q',121 <FLY>
A:Cross-references: UNIPARC:UPI0001733AD
R:Nakao, K.; Itoh, H.; Kambayashi, Y.; Hosoda, K.; Saito, Y.; Yamada, T.; Mukoyama, M.; Hypertension 15, 774-778, 1990
A>Title: Rat brain natriuretic peptide. Isolation from rat heart and tissue distribution
A:Reference number: A60735; MUID:90277148; PMID:2351430
A:Accession: A60735
A:Molecule type: protein
A:Residues: 77-121 <NAK>
A:Cross-references: UNIPARC:UPI000003520F
R:Dagnino, L.; Drouin, J.; Nemer, M. Mol. Endocrinol. 5, 1292-1300, 1991
A>Title: Differential expression of natriuretic peptide genes in cardiac and extracardiac
A:Reference number: I57704; MUID:92123224; PMID:1837590
A:Accession: I57704
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-121 <RES>
A:Cross-references: UNIPARC:UPI0000125ADC; GB:M60266; NID:G204983; PIDN:AAA41455.1; PID: C:Genetics:
A:Introns: 42/3; 117/1
C:Superfamily: natriuretic peptide A precursor
C:Keywords: cardiac muscle; heart
F:1-26/Domain: signal sequence
F:27-121/Product: brain natriuretic factor #status experimental <MAT1>
F:77-121/Product: brain natriuretic factor BNP-45 #status experimental <MAT2>
Query Match 68.5%; Score 63; DB 1; Length 121;
Best Local Similarity 64.7%; Pred. No. 0.0011;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
||||:||||:||||
DB 99 CFGRKIDRIGAVSRLLGC 115
RESULT 38
AH3254
acetyl-CoA:acetoacetyl-CoA transferase alpha chain (EC 2.8.3.-) [imported] - Brucella melitensis
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AH3254
R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Loz, T.; Ivanova, .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AH3254
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-496 <KUR>
A:Cross-references: UNIPROT:Q8YJR1; UNIPARC:UPI0000057B02; GB:AE008917; PIDN:AAL51203.1; A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0021
A:Map position: I
C:Keywords: CoA-transferase
Query Match 47.8%; Score 44; DB 2; Length 496;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 9 ISSSSGLGC 17
:|||||
DB 22 VSSSSGLGC 30
RESULT 39
H86463

F12G12.17 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86463
A:Residues: 77-119,'Q',121 <FLY>
A:Cross-references: UNIPARC:UPI0001733AD
R:Nakao, K.; Itoh, H.; Kambayashi, Y.; Hosoda, K.; Saito, Y.; Yamada, T.; Mukoyama, M.; Hypertension 15, 774-778, 1990
A>Title: Rat brain natriuretic peptide. Isolation from rat heart and tissue distribution
A:Reference number: A60735; MUID:90277148; PMID:2351430
A:Accession: A60735
A:Molecule type: protein
A:Residues: 77-121 <NAK>
A:Cross-references: UNIPARC:UPI000003520F
R:Dagnino, L.; Drouin, J.; Nemer, M. Mol. Endocrinol. 5, 1292-1300, 1991
A>Title: Differential expression of natriuretic peptide genes in cardiac and extracardiac
A:Reference number: I57704; MUID:92123224; PMID:1837590
A:Accession: I57704
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-121 <RES>
A:Cross-references: UNIPARC:UPI0000125ADC; GB:M60266; NID:G204983; PIDN:AAA41455.1; PID: C:Genetics:
A:Introns: 42/3; 117/1
C:Superfamily: natriuretic peptide A precursor
C:Keywords: cardiac muscle; heart
F:1-26/Domain: signal sequence
F:27-121/Product: brain natriuretic factor #status experimental <MAT1>
F:77-121/Product: brain natriuretic factor BNP-45 #status experimental <MAT2>
Query Match 46.7%; Score 43; DB 2; Length 231;
Best Local Similarity 63.6%; Pred. No. 7.6;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CFGRKMDRISS 11
||||:||||:||||
DB 139 CFGRKSRLES 149
RESULT 40
T24265
hypothetical protein T01B4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24265
R:Wilkinson, J.
A:Reference number: Z19866
A:Accession: T24265
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-522 <WIL>
A:Cross-references: UNIPROT:Q22042; UNIPARC:UPI000007D5F5; EMBL:Z70036; PIDN:CAA93875.1
A:Experimental source: clone T01B4
C:Genetics:
A:Gene: CBSP:T01B4.1
A:Map position: X
A:Introns: 95/3; 142/1; 224/3; 290/1; 458/1
Query Match 46.7%; Score 43; DB 2; Length 522;
Best Local Similarity 53.3%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGL 15
||||:||||:||||
DB 197 CFGRKQKRASSLASI 211
RESULT 41
F64593
pyruvate synthase (EC 1.2.7.1) beta chain - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C:Accession: F64593
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen, son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C

A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: F64593
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-273 <TOM>
A:Cross-references: UNIPROT:O25312; UNIPARC:UPI00000D3008; GB:AE000572; GB:AE000511; NID:
C:Superfamily: 2-oxoacid:ferredoxin oxidoreductase, beta subunit
C:Keywords: coenzyme A; oxidoreductase

Query Match 45.7%; Score 42; DB 1; Length 273;
Best Local Similarity 53.3%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 GRKMDRISSSSGLG 17
| | | | : | | | |
DB 39 GWKMDVCLVSGTGC 53
| | | | : | | | |

RESULT 42
H71919
chain of 2-oxoglutarate oxidoreductase - *Helicobacter pylori* (strain J99)
C:Species: *Helicobacter pylori*
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Oct-2004
C:Accession: H71919
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:99233682
A:Accession: H71919
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-273 <ARN>
A:Cross-references: UNIPROT:O9ZLP0; UNIPARC:UPI00000D364F; GB:AE001486; GB:AE001439; NID:
A:Experimental source: strain J99
C:Genetics:
C:Superfamily: 2-oxoacid:ferredoxin oxidoreductase, beta subunit

Query Match 45.7%; Score 42; DB 2; Length 273;
Best Local Similarity 53.3%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 GRKMDRISSSSGLG 17
| | | | : | | | |
DB 39 GWKMDVCLVSGTGC 53
| | | | : | | | |

RESULT 43
T51402
serine/threonine-specific protein kinase-like protein - *Arabidopsis thaliana*
N:Alternate names: protein F14F8_110
C:Species: *Arabidopsis thaliana* (mouse-ear cross)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 05-Oct-2004
C:Accession: T51402
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25394
A:Accession: T51402
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-436 <SAT>
A:Cross-references: UNIPROT:Q9LFV3; UNIPARC:UPI0000048B47; EMBL:AL391144
A:Experimental source: cultivar Columbia; BAC clone F14F8
C:Genetics:
A:Map position: 5
A:Introns: 107/2; 158/3; 202/1; 254/3; 322/3
A>Note: F14F8_110

Query Match 45.7%; Score 42; DB 2; Length 436;
Best Local Similarity 57.1%; Pred. No. 22;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 GRKMDRISSSSGLG 16
| | | | : | | | |
DB 385 GRRQDTMSSSFGVG 398
| | | | : | | | |

RESULT 44
D64760
yahr protein - *Escherichia coli* (strain K-12)
C:Species: *Escherichia coli*
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: D64760
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: D64760
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-148 <BLAT>
A:Cross-references: UNIPROT:O65941; UNIPARC:UPI00000C0A32; GB:AE000140; GB:U000096; NID:
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: yahr
C:Superfamily: *Escherichia coli* yahr protein

Query Match 44.6%; Score 41; DB 2; Length 148;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 MDRISSSSGLG 17
| | | | : | | | |
DB 19 ISRVSGASGIGC 30
| | | | : | | | |

RESULT 45
T41462
transcription regulator - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41462
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z21996
A:Accession: T41462
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-307 <LYN>
A:Cross-references: UNIPROT:O14311; UNIPARC:UPI0000135E92; EMBL:AL034381; PIDN:CAA22271
A:Experimental source: strain 972h-; cosmid c61
C:Genetics:
A:Gene: SPDB:SPCC61.02
A:Map position: 3
C:Superfamily: transcription regulator SPCC61.02

Query Match 44.6%; Score 41; DB 2; Length 307;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 RMDRISSSSGLG 16
| | | | : | | | |
DB 235 RMDRIQSSSGSG 246
| | | | : | | | |

RESULT 46
B95358
probable acyl-CoA transferase (EC 2.8.3.-) [imported] - *Sinorhizobium meliloti* (strain
C:Species: *Sinorhizobium meliloti*
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95358
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abolia, A.P.; Barloy-Hubler, F.; Bow;

.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: B95358
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-523 <KUR>
A:Cross-references: UNIPROT:Q92YU3; UNIPARC:UPI00000CB1D1; GB:AE006459; PIDN:AAK65428.1;
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubier, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, H.; Vandenbol, M.; Vorholter, P.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMal409
A:Genome: plasmid
C:Keywords: CoA-transferase
Query Match 44.6%; Score 41; DB 2; Length 523;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 9 ISSSSGLG 17
Db 22 VNSSSGLG 30
RESULT 47
E87627
hypothetical protein CC3055 [imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
A:Accession: E87627
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87627
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-738 <STO>
A:Cross-references: UNIPROT:Q9A3Z5; UNIPARC:UPI00000C7933; GB:AE005673; NID:gl3424701; F
C:Genetics:
A:Gene: CC3055
Query Match 44.6%; Score 41; DB 2; Length 738;
Best Local Similarity 64.3%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CFGKMDRISSSSG 14
Db 695 CFGVKPSASSSG 708
RESULT 48
S74219
alpha-galactosidase (EC 3.2.1.22) II precursor - fungus (*Trichoderma reesei*)
C:Species: *Trichoderma reesei*
C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
A:Accession: S74219
R:Margolles-Clark, E.; Tenkanen, M.; Luonteri, E.; Penttilae, M. Eur. J. Biochem. 240, 104-111, 1996
A:Title: Three alpha-galactosidase genes of *Trichoderma reesei* cloned by expression in *Y*
A:Reference number: S74218; MUID:96330869; PMID:8797842
A:Accession: S74219

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-746 <MAR>
A:Cross-references: UNIPROT:Q92457; UNIPARC:UPI000006A7AC; EMBL:Z69254; NID:gl580817; P1
C:Genetics:
A:Gene: agl2
C:Superfamily: alpha-galactosidase II
C:Keywords: glycoprotein; glycosidase; hydrolase
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-746/Product: alpha-galactosidase II #status predicted <MAT>
F:43,156,180,188,360,427,446,495,714/Binding site: carboxydrate (Asn) (covalent) #status
Query Match 44.6%; Score 41; DB 2; Length 746;
Best Local Similarity 53.3%; Pred. No. 57;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 2 FGKMDRISSSSGLG 16
Db 386 FGKHPRVSDNAGLG 400
RESULT 49
AF1755
bacteriophage protein homolog lin2587 [imported] - *Listeria innocua* (strain Clip11262)
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
A:Accession: AF1755
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Welland, A. Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1755
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-757 <GLA>
A:Cross-references: UNIPROT:Q92BE8; UNIPARC:UPI00000CC901; GB:AL592022; PIDN:CAC97814.1;
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin2587
Query Match 44.6%; Score 41; DB 2; Length 757;
Best Local Similarity 60.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CFGKMDRISSSSGL 15
Db 242 CNAKMDLFRSSGL 256
RESULT 50
H83190
Probable outer membrane protein PA3648 [imported] - *Pseudomonas aeruginosa* (strain PAO1)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
A:Accession: H83190
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, L.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic path
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: H83190
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-797 <STO>
A:Cross-references: UNIPROT:Q9HYX4; UNIPARC:UPI00000C5AA3; GB:AE004784; GB:AE004091; NID
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA3648

C;Superfamily: protective surface antigen D-15

Query Match 44.6%; Score 41; DB 2; Length 797;
Best Local Similarity 50.0%; Pred. NO. 61;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSLG 16
Db 745 CDGKTDNLASSVG 760

Search completed: January 25, 2006, 18:48:18
Job time : 35 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 25, 2006, 18:44:48 ; Search time 62 Seconds
(without alignments)
114.566 Million cell updates/sec

Title: US-10-737-290-172
Perfect score: 92
Sequence: 1 CPGKXWDRISSSGLGC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	17	4	US-10-723-933-128
2	92	100.0	17	5	US-10-737-290-172
3	92	100.0	18	4	US-10-723-933-129
4	92	100.0	18	5	US-10-471-348-44
5	92	100.0	18	6	US-11-040-810-44
6	92	100.0	23	4	US-10-723-933-130
7	92	100.0	23	5	US-10-471-348-31
8	92	100.0	23	6	US-11-040-810-31
9	92	100.0	24	4	US-10-723-933-127
10	92	100.0	24	5	US-10-471-348-33
11	92	100.0	24	6	US-11-040-810-33
12	92	100.0	25	5	US-10-471-348-22
13	92	100.0	25	6	US-10-471-348-24
14	92	100.0	25	6	US-11-040-810-22
15	92	100.0	25	6	US-11-040-810-24
16	92	100.0	26	3	US-09-902-517-1
17	92	100.0	26	4	US-10-106-806-7
18	92	100.0	26	4	US-10-402-021-1
19	92	100.0	26	4	US-10-723-933-107
20	92	100.0	26	4	US-10-723-933-124
21	92	100.0	26	5	US-10-947-730-7
22	92	100.0	29	4	US-10-723-933-106
23	92	100.0	29	4	US-10-723-933-123
24	92	100.0	32	3	US-09-752-724-4
25	92	100.0	32	3	US-09-466-268B-6
26	92	100.0	32	3	US-09-902-517-49
27	92	100.0	32	4	US-10-106-806-6

28	92	100.0	32	4	US-10-197-954-24	Sequence 24, Appl
29	92	100.0	32	4	US-10-402-021-49	Sequence 49, Appl
30	92	100.0	32	4	US-10-664-605-4	Sequence 4, Appl
31	92	100.0	32	4	US-10-723-933-33	Sequence 33, Appl
32	92	100.0	32	4	US-10-723-933-53	Sequence 53, Appl
33	92	100.0	32	4	US-10-723-933-73	Sequence 73, Appl
34	92	100.0	32	4	US-10-723-933-110	Sequence 110, Appl
35	92	100.0	32	4	US-10-723-933-111	Sequence 111, Appl
36	92	100.0	32	5	US-10-818-246-5	Sequence 5, Appl
37	92	100.0	32	5	US-10-471-348-21	Sequence 21, Appl
38	92	100.0	32	5	US-10-471-348-54	Sequence 54, Appl
39	92	100.0	32	5	US-10-760-085-24	Sequence 24, Appl
40	92	100.0	32	5	US-10-947-730-6	Sequence 6, Appl
41	92	100.0	32	5	US-10-989-397-2	Sequence 2, Appl
42	92	100.0	32	5	US-10-775-204-1802	Sequence 1802, Ap
43	92	100.0	32	6	US-11-040-810-21	Sequence 21, Appl
44	92	100.0	32	6	US-11-040-810-54	Sequence 54, Appl
45	92	100.0	32	6	US-11-066-697-509	Sequence 509, App
46	92	100.0	32	6	US-11-066-697-516	Sequence 516, App
47	92	100.0	33	3	US-09-942-709-1	Sequence 1, Appl
48	92	100.0	33	4	US-10-723-933-112	Sequence 112, App
49	92	100.0	33	5	US-10-697-886-1	Sequence 1, Appl
50	92	100.0	33	5	US-10-471-348-55	Sequence 55, Appl
51	92	100.0	33	6	US-11-040-810-55	Sequence 55, Appl
52	92	100.0	36	4	US-10-723-933-80	Sequence 80, Appl
53	92	100.0	41	3	US-09-466-268B-1	Sequence 1, Appl
54	92	100.0	41	4	US-10-106-806-1	Sequence 1, Appl
55	92	100.0	41	5	US-10-947-730-1	Sequence 1, Appl
56	92	100.0	108	4	US-10-419-059-1	Sequence 1, Appl
57	92	100.0	108	4	US-10-300-733-1	Sequence 1, Appl
58	92	100.0	108	4	US-10-359-051-1	Sequence 1, Appl
59	92	100.0	108	4	US-10-645-874-1	Sequence 1, Appl
60	92	100.0	108	5	US-10-714-078-1	Sequence 1, Appl
61	92	100.0	108	5	US-10-603-891-1	Sequence 1, Appl
62	92	100.0	108	5	US-10-827-919-1	Sequence 1, Appl
63	92	100.0	108	5	US-10-938-760-1	Sequence 1, Appl
64	92	100.0	108	5	US-10-952-275-1	Sequence 1, Appl
65	92	100.0	134	3	US-09-902-517-45	Sequence 45, Appl
66	92	100.0	134	3	US-09-902-517-48	Sequence 48, Appl
67	92	100.0	134	3	US-09-508-435-2	Sequence 2, Appl
68	92	100.0	134	4	US-10-419-059-2	Sequence 2, Appl
69	92	100.0	134	4	US-10-402-021-45	Sequence 45, Appl
70	92	100.0	134	4	US-10-402-021-48	Sequence 48, Appl
71	92	100.0	134	4	US-10-645-874-2	Sequence 2, Appl
72	92	100.0	134	4	US-10-723-933-22	Sequence 22, Appl
73	92	100.0	134	5	US-10-714-078-2	Sequence 2, Appl
74	92	100.0	134	5	US-10-603-891-2	Sequence 2, Appl
75	92	100.0	134	5	US-10-827-919-2	Sequence 2, Appl
76	92	100.0	134	5	US-10-952-275-2	Sequence 2, Appl
77	92	100.0	134	5	US-10-775-204-1277	Sequence 1277, Ap
78	92	100.0	195	4	US-10-723-933-115	Sequence 115, App
79	92	100.0	641	5	US-10-775-204-1634	Sequence 1634, Ap
80	92	100.0	719	5	US-10-775-204-1275	Sequence 1275, Ap
81	90	97.8	33	6	US-11-066-697-515	Sequence 515, App
82	89	96.7	19	4	US-10-723-933-84	Sequence 84, Appl
83	89	96.7	32	5	US-10-471-348-48	Sequence 48, Appl
84	89	96.7	32	6	US-10-471-348-49	Sequence 49, Appl
85	89	96.7	32	6	US-11-040-810-48	Sequence 48, Appl
86	89	96.7	32	6	US-11-040-810-49	Sequence 49, Appl
87	89	96.7	33	4	US-10-723-933-108	Sequence 108, App
88	89	96.7	33	5	US-10-471-348-50	Sequence 50, Appl
89	89	96.7	33	6	US-11-040-810-50	Sequence 50, Appl
90	88	95.7	18	5	US-10-471-348-41	Sequence 41, Appl
91	88	95.7	18	6	US-11-040-810-41	Sequence 41, Appl
92	88	95.7	23	5	US-10-471-348-28	Sequence 28, Appl
93	88	95.7	23	6	US-11-040-810-28	Sequence 28, Appl
94	88	95.7	24	6	US-10-471-348-30	Sequence 30, Appl
95	88	95.7	24	6	US-11-040-810-30	Sequence 30, Appl
96	88	95.7	25	5	US-10-471-348-25	Sequence 25, Appl
97	88	95.7	25	5	US-10-471-348-26	Sequence 26, Appl
98	88	95.7	25	6	US-11-040-810-25	Sequence 25, Appl
99	88	95.7	25	6	US-11-040-810-26	Sequence 26, Appl
100	88	95.7	26	5	US-10-471-348-27	Sequence 27, Appl

101	88	95.7	26	6	US-11-040-810-27	Sequence 27, Appl	174	76	82.6	131	4	US-10-402-021-43	Sequence 43, Appl
102	88	95.7	32	5	US-10-471-348-45	Sequence 45, Appl	175	76	82.6	131	4	US-10-402-021-46	Sequence 46, Appl
103	88	95.7	32	5	US-10-471-348-46	Sequence 46, Appl	176	76	82.6	132	3	US-09-902-517-47	Sequence 47, Appl
104	88	95.7	32	5	US-10-471-348-57	Sequence 57, Appl	177	76	82.6	132	4	US-10-402-021-47	Sequence 47, Appl
105	88	95.7	32	6	US-11-040-810-45	Sequence 45, Appl	178	75	81.5	17	4	US-10-664-605-10	Sequence 10, Appl
106	88	95.7	32	6	US-11-040-810-46	Sequence 46, Appl	179	74	80.4	17	4	US-10-664-605-40	Sequence 40, Appl
107	88	95.7	32	6	US-11-040-810-57	Sequence 57, Appl	180	74	80.4	17	4	US-10-664-605-67	Sequence 67, Appl
108	88	95.7	33	5	US-10-471-348-47	Sequence 47, Appl	181	74	80.4	17	4	US-10-664-605-69	Sequence 69, Appl
109	88	95.7	33	5	US-11-040-810-47	Sequence 47, Appl	182	74	80.4	17	5	US-10-471-348-43	Sequence 43, Appl
110	86	93.5	17	4	US-10-723-933-1	Sequence 1, Appl	183	74	80.4	17	6	US-11-040-810-43	Sequence 43, Appl
111	86	93.5	17	4	US-10-723-933-79	Sequence 79, Appl	184	73	79.3	17	4	US-10-327-514-19	Sequence 19, Appl
112	86	93.5	18	4	US-10-723-933-21	Sequence 21, Appl	185	73	79.3	17	4	US-10-664-605-2	Sequence 2, Appl
113	86	93.5	25	4	US-10-723-933-126	Sequence 126, Appl	186	73	79.3	17	4	US-10-664-605-66	Sequence 66, Appl
114	86	93.5	25	4	US-10-723-933-116	Sequence 116, Appl	187	73	79.3	17	4	US-10-499-762-19	Sequence 19, Appl
115	86	93.5	29	4	US-10-723-933-82	Sequence 82, Appl	188	73	79.3	22	3	US-09-752-724-9	Sequence 9, Appl
116	86	93.5	32	4	US-10-723-933-83	Sequence 83, Appl	189	73	79.3	22	3	US-09-912-425-3	Sequence 3, Appl
117	86	93.5	32	4	US-10-723-933-131	Sequence 131, Appl	190	73	79.3	22	4	US-10-106-806-9	Sequence 9, Appl
118	86	93.5	32	5	US-10-723-933-131	Sequence 131, Appl	191	73	79.3	22	4	US-10-106-806-1	Sequence 1, Appl
119	86	93.5	32	5	US-10-471-348-56	Sequence 56, Appl	192	73	79.3	22	4	US-10-664-605-1	Sequence 1, Appl
120	86	93.5	32	6	US-11-040-810-56	Sequence 56, Appl	193	73	79.3	22	5	US-10-947-730-8	Sequence 8, Appl
121	86	93.5	33	4	US-10-723-933-5	Sequence 5, Appl	194	73	79.3	22	5	US-10-947-730-9	Sequence 9, Appl
122	86	93.5	37	4	US-10-723-933-117	Sequence 117, Appl	195	73	79.3	22	5	US-10-989-397-3	Sequence 3, Appl
123	85	92.4	23	5	US-10-471-348-34	Sequence 34, Appl	196	73	79.3	22	5	US-10-989-397-3	Sequence 3, Appl
124	85	92.4	23	5	US-10-471-348-35	Sequence 35, Appl	197	73	79.3	22	5	US-10-989-397-3	Sequence 3, Appl
125	85	92.4	23	6	US-11-040-810-34	Sequence 34, Appl	198	73	79.3	22	6	US-11-066-697-517	Sequence 517, Appl
126	85	92.4	23	6	US-11-040-810-35	Sequence 35, Appl	199	73	79.3	23	6	US-11-066-697-524	Sequence 524, Appl
127	85	92.4	24	6	US-10-471-348-36	Sequence 36, Appl	200	73	79.3	27	4	US-10-360-101-25	Sequence 25, Appl
128	85	92.4	24	6	US-11-040-810-36	Sequence 36, Appl	201	73	79.3	27	4	US-10-360-101-88	Sequence 88, Appl
129	85	92.4	32	5	US-10-471-348-37	Sequence 37, Appl	202	73	79.3	27	5	US-10-760-085-142	Sequence 142, Appl
130	85	92.4	32	5	US-10-471-348-51	Sequence 51, Appl	203	73	79.3	27	6	US-11-066-697-523	Sequence 523, Appl
131	85	92.4	32	6	US-11-040-810-37	Sequence 37, Appl	204	73	79.3	27	6	US-11-066-697-523	Sequence 523, Appl
132	85	92.4	32	6	US-11-040-810-51	Sequence 51, Appl	205	73	79.3	29	6	US-09-752-724-8	Sequence 8, Appl
133	85	92.4	32	6	US-11-040-810-52	Sequence 52, Appl	206	73	79.3	29	6	US-11-066-697-465	Sequence 465, Appl
134	85	92.4	33	5	US-10-471-348-38	Sequence 38, Appl	207	73	79.3	37	3	US-09-466-268B-2	Sequence 2, Appl
135	85	92.4	33	5	US-10-471-348-53	Sequence 53, Appl	208	73	79.3	37	3	US-10-106-806-2	Sequence 2, Appl
136	85	92.4	33	5	US-11-040-810-38	Sequence 38, Appl	209	73	79.3	37	5	US-10-947-730-2	Sequence 2, Appl
137	85	92.4	33	6	US-11-040-810-53	Sequence 53, Appl	210	73	79.3	37	5	US-10-360-101-87	Sequence 87, Appl
138	85	92.4	33	6	US-11-040-810-58	Sequence 58, Appl	211	73	79.3	53	6	US-11-066-697-519	Sequence 519, Appl
139	83	90.2	17	6	US-10-471-348-42	Sequence 42, Appl	212	73	79.3	53	6	US-11-066-697-520	Sequence 520, Appl
140	83	90.2	17	6	US-11-040-810-42	Sequence 42, Appl	213	73	79.3	103	3	US-09-912-425-2	Sequence 2, Appl
141	83	90.2	23	5	US-10-471-348-32	Sequence 32, Appl	214	73	79.3	126	3	US-09-912-425-1	Sequence 1, Appl
142	83	90.2	23	6	US-11-040-810-32	Sequence 32, Appl	215	73	79.3	126	4	US-10-645-874-5	Sequence 5, Appl
143	83	90.2	23	6	US-09-466-268B-7	Sequence 7, Appl	216	73	79.3	126	4	US-10-645-874-5	Sequence 5, Appl
144	81	88.0	32	4	US-10-360-101-86	Sequence 86, Appl	217	73	79.3	126	5	US-10-827-913-5	Sequence 35, Appl
145	81	88.0	32	4	US-10-723-933-132	Sequence 132, Appl	218	73	79.3	126	5	US-10-737-318-35	Sequence 38, Appl
146	79	85.9	17	5	US-10-471-348-39	Sequence 39, Appl	219	73	79.3	152	5	US-10-982-514-16	Sequence 16, Appl
147	79	85.9	17	6	US-11-040-810-39	Sequence 39, Appl	220	73	79.3	157	5	US-10-982-514-17	Sequence 17, Appl
148	79	85.9	23	5	US-10-471-348-29	Sequence 29, Appl	221	73	79.3	17	3	US-09-902-517-5	Sequence 5, Appl
149	79	85.9	23	6	US-11-040-810-29	Sequence 29, Appl	222	72	78.3	17	4	US-10-402-021-5	Sequence 5, Appl
150	78	84.8	17	4	US-10-664-605-68	Sequence 68, Appl	223	72	78.3	17	4	US-10-664-605-41	Sequence 41, Appl
151	76	82.6	17	3	US-09-902-517-15	Sequence 15, Appl	224	72	78.3	17	4	US-10-664-605-42	Sequence 42, Appl
152	76	82.6	17	4	US-10-402-021-15	Sequence 15, Appl	225	72	78.3	17	4	US-10-664-605-46	Sequence 46, Appl
153	76	82.6	20	3	US-09-902-517-34	Sequence 34, Appl	226	72	78.3	17	4	US-10-664-605-47	Sequence 47, Appl
154	76	82.6	20	4	US-10-402-021-34	Sequence 34, Appl	227	72	78.3	17	4	US-10-664-605-52	Sequence 52, Appl
155	76	82.6	26	3	US-09-902-517-3	Sequence 3, Appl	228	72	78.3	17	4	US-10-664-605-52	Sequence 52, Appl
156	76	82.6	26	4	US-10-402-021-3	Sequence 3, Appl	229	72	78.3	22	3	US-09-752-724-10	Sequence 10, Appl
157	76	82.6	26	4	US-10-723-933-35	Sequence 35, Appl	230	72	78.3	22	6	US-11-066-697-508	Sequence 508, Appl
158	76	82.6	26	4	US-10-723-933-51	Sequence 51, Appl	231	72	78.3	22	6	US-11-066-697-518	Sequence 518, Appl
159	76	82.6	26	6	US-09-752-724-6	Sequence 6, Appl	232	72	78.3	27	6	US-11-066-697-482	Sequence 482, Appl
160	76	82.6	32	3	US-09-752-724-6	Sequence 75, Appl	233	72	78.3	27	6	US-11-066-697-491	Sequence 491, Appl
161	76	82.6	32	4	US-10-723-933-137	Sequence 137, Appl	234	72	78.3	27	6	US-11-066-697-501	Sequence 501, Appl
162	76	82.6	32	4	US-10-723-933-137	Sequence 137, Appl	235	71	77.2	17	3	US-09-027-777B-1	Sequence 1, Appl
163	76	82.6	32	6	US-11-066-697-507	Sequence 507, Appl	236	71	77.2	17	4	US-10-664-605-51	Sequence 51, Appl
164	76	82.6	32	6	US-11-066-697-512	Sequence 512, Appl	237	71	77.2	17	4	US-10-664-605-62	Sequence 62, Appl
165	76	82.6	41	3	US-09-902-517-50	Sequence 50, Appl	238	71	77.2	17	6	US-11-066-697-474	Sequence 474, Appl
166	76	82.6	106	3	US-09-902-517-30	Sequence 30, Appl	239	71	77.2	20	3	US-09-902-517-32	Sequence 32, Appl
167	76	82.6	131	3	US-10-402-021-30	Sequence 30, Appl	240	71	77.2	20	4	US-10-402-021-32	Sequence 32, Appl
168	76	82.6	131	3	US-09-902-517-39	Sequence 39, Appl	241	71	77.2	22	3	US-09-752-724-3	Sequence 3, Appl
169	76	82.6	131	3	US-09-902-517-41	Sequence 41, Appl	242	71	77.2	22	5	US-10-471-348-17	Sequence 17, Appl
170	76	82.6	131	3	US-09-902-517-43	Sequence 43, Appl	243	71	77.2	22	6	US-11-040-810-17	Sequence 17, Appl
171	76	82.6	131	3	US-09-902-517-46	Sequence 46, Appl	244	71	77.2	22	6	US-11-066-697-475	Sequence 475, Appl
172	76	82.6	131	4	US-10-402-021-39	Sequence 39, Appl	245	71	77.2	23	6	US-11-066-697-481	Sequence 481, Appl
173	76	82.6	131	4	US-10-402-021-41	Sequence 41, Appl	246	71	77.2	23	6	US-11-066-697-481	Sequence 481, Appl

247	71	77.2	24	5	US-10-471-348-15	Sequence 15, Appl	320	70	76.1	17	4	US-10-723-933-109	Sequence 109, App
248	71	77.2	24	5	US-10-471-348-16	Sequence 16, Appl	321	70	76.1	17	5	US-10-471-348-40	Sequence 40, Appl
249	71	77.2	24	6	US-11-040-810-15	Sequence 15, Appl	322	70	76.1	17	6	US-11-040-810-40	Sequence 40, Appl
250	71	77.2	24	6	US-11-040-810-16	Sequence 16, Appl	323	70	76.1	28	5	US-10-471-348-6	Sequence 6, Appl
251	71	77.2	24	6	US-11-066-697-473	Sequence 473, App	324	70	76.1	28	6	US-11-040-810-6	Sequence 6, Appl
252	71	77.2	25	3	US-09-502-517-2	Sequence 2, Appl	325	70	76.1	37	4	US-10-723-933-136	Sequence 136, App
253	71	77.2	25	4	US-10-402-021-2	Sequence 2, Appl	326	69	75.0	37	4	US-10-664-605-35	Sequence 35, Appl
254	71	77.2	25	4	US-10-156-527-16	Sequence 16, Appl	327	69	75.0	17	4	US-10-664-605-50	Sequence 50, Appl
255	71	77.2	26	6	US-11-066-697-480	Sequence 480, App	328	69	75.0	17	4	US-10-664-605-55	Sequence 55, Appl
256	71	77.2	26	6	US-11-066-697-479	Sequence 479, App	329	69	75.0	196	4	US-10-201-288-2	Sequence 2, Appl
257	71	77.2	28	3	US-09-752-724-1	Sequence 1, Appl	330	69	75.0	196	5	US-10-919-325-2	Sequence 2, Appl
258	71	77.2	28	3	US-09-466-268B-5	Sequence 5, Appl	331	69	75.0	265	5	US-10-471-931-2	Sequence 2, Appl
259	71	77.2	28	4	US-10-106-806-5	Sequence 5, Appl	332	68	73.9	17	4	US-10-664-605-9	Sequence 9, Appl
260	71	77.2	28	4	US-10-197-954-14	Sequence 14, Appl	333	68	73.9	17	4	US-10-664-605-31	Sequence 31, Appl
261	71	77.2	28	4	US-10-279-061-1	Sequence 1, Appl	334	68	73.9	17	4	US-10-664-605-37	Sequence 37, Appl
262	71	77.2	28	4	US-10-279-061-76	Sequence 76, Appl	335	68	73.9	17	4	US-10-664-605-48	Sequence 48, Appl
263	71	77.2	28	4	US-10-360-101-84	Sequence 84, Appl	336	68	73.9	17	4	US-10-664-605-53	Sequence 53, Appl
264	71	77.2	28	5	US-10-471-348-1	Sequence 1, Appl	337	68	73.9	17	4	US-10-664-605-63	Sequence 63, Appl
265	71	77.2	28	5	US-10-471-348-2	Sequence 2, Appl	338	68	73.9	17	4	US-10-664-605-70	Sequence 70, Appl
266	71	77.2	28	5	US-10-471-348-3	Sequence 3, Appl	339	68	73.9	22	3	US-09-752-724-11	Sequence 11, Appl
267	71	77.2	28	5	US-10-471-348-4	Sequence 4, Appl	340	68	73.9	28	5	US-10-471-348-12	Sequence 12, Appl
268	71	77.2	28	5	US-10-718-071-20	Sequence 20, Appl	341	68	73.9	28	6	US-11-040-810-12	Sequence 12, Appl
269	71	77.2	28	5	US-10-718-071-41	Sequence 41, Appl	342	67	72.8	17	4	US-10-327-514-17	Sequence 17, Appl
270	71	77.2	28	5	US-10-760-085-14	Sequence 14, Appl	343	67	72.8	17	4	US-10-664-605-8	Sequence 8, Appl
271	71	77.2	28	5	US-10-947-730-5	Sequence 5, Appl	344	67	72.8	17	4	US-10-664-605-25	Sequence 25, Appl
272	71	77.2	28	5	US-10-989-397-1	Sequence 1, Appl	345	67	72.8	17	4	US-10-664-605-26	Sequence 26, Appl
273	71	77.2	28	5	US-10-775-204-2207	Sequence 2207, Ap	346	67	72.8	17	4	US-10-664-605-28	Sequence 28, Appl
274	71	77.2	28	6	US-11-040-810-1	Sequence 1, Appl	347	67	72.8	17	4	US-10-664-605-29	Sequence 29, Appl
275	71	77.2	28	6	US-11-040-810-2	Sequence 2, Appl	348	67	72.8	17	4	US-10-664-605-30	Sequence 30, Appl
276	71	77.2	28	6	US-11-040-810-3	Sequence 3, Appl	349	67	72.8	17	4	US-10-664-605-36	Sequence 36, Appl
277	71	77.2	28	6	US-11-040-810-4	Sequence 4, Appl	350	67	72.8	17	4	US-10-664-605-44	Sequence 44, Appl
278	71	77.2	28	6	US-11-066-697-476	Sequence 476, App	351	67	72.8	17	4	US-10-664-605-58	Sequence 58, Appl
279	71	77.2	28	6	US-11-066-697-495	Sequence 495, App	352	67	72.8	17	4	US-10-664-605-61	Sequence 61, Appl
280	71	77.2	29	3	US-09-772-607-9	Sequence 9, Appl	353	67	72.8	17	4	US-10-664-605-71	Sequence 71, Appl
281	71	77.2	29	3	US-09-772-607-9	Sequence 9, Appl	354	67	72.8	17	5	US-10-499-762-17	Sequence 17, Appl
282	71	77.2	29	4	US-10-664-605-3	Sequence 3, Appl	355	67	72.8	21	6	US-11-066-697-483	Sequence 483, App
283	71	77.2	29	5	US-10-471-348-5	Sequence 5, Appl	356	67	72.8	22	5	US-10-471-348-13	Sequence 13, Appl
284	71	77.2	29	6	US-11-040-810-5	Sequence 5, Appl	357	67	72.8	22	5	US-10-471-348-23	Sequence 23, Appl
285	71	77.2	31	3	US-09-964-201A-22	Sequence 22, Appl	358	67	72.8	22	6	US-11-040-810-13	Sequence 13, Appl
286	71	77.2	31	4	US-10-681-389-22	Sequence 22, Appl	359	67	72.8	22	6	US-11-040-810-23	Sequence 23, Appl
287	71	77.2	31	4	US-10-681-388-22	Sequence 22, Appl	360	67	72.8	23	6	US-11-066-697-484	Sequence 484, App
288	71	77.2	32	3	US-09-027-777B-5	Sequence 5, Appl	361	67	72.8	24	6	US-11-066-697-485	Sequence 485, App
289	71	77.2	32	3	US-09-027-777B-10	Sequence 10, Appl	362	67	72.8	24	6	US-11-066-697-487	Sequence 487, App
290	71	77.2	32	3	US-09-027-777B-11	Sequence 11, Appl	363	67	72.8	24	6	US-11-066-697-502	Sequence 502, App
291	71	77.2	32	4	US-10-723-933-74	Sequence 74, Appl	364	67	72.8	24	6	US-11-066-697-505	Sequence 505, App
292	71	77.2	32	5	US-10-471-348-8	Sequence 8, Appl	365	67	72.8	25	6	US-11-066-697-488	Sequence 488, App
293	71	77.2	32	5	US-10-471-348-9	Sequence 9, Appl	366	67	72.8	26	6	US-10-723-933-113	Sequence 113, App
294	71	77.2	32	5	US-10-471-348-10	Sequence 10, Appl	367	67	72.8	26	6	US-11-066-697-478	Sequence 478, App
295	71	77.2	32	5	US-10-989-397-4	Sequence 4, Appl	368	67	72.8	28	3	US-09-752-724-2	Sequence 2, Appl
296	71	77.2	32	5	US-10-775-204-2203	Sequence 2203, Ap	369	67	72.8	28	6	US-11-066-697-486	Sequence 486, App
297	71	77.2	32	6	US-11-040-810-8	Sequence 8, Appl	370	67	72.8	32	6	US-11-066-697-490	Sequence 490, App
298	71	77.2	32	6	US-11-040-810-9	Sequence 9, Appl	371	66	71.7	17	4	US-10-664-605-32	Sequence 32, Appl
299	71	77.2	32	6	US-11-040-810-10	Sequence 10, Appl	372	66	71.7	17	4	US-10-664-605-33	Sequence 33, Appl
300	71	77.2	32	6	US-11-066-697-504	Sequence 504, App	373	66	71.7	17	4	US-10-664-605-43	Sequence 43, Appl
301	71	77.2	37	3	US-09-027-777B-4	Sequence 4, Appl	374	66	71.7	20	6	US-11-066-697-469	Sequence 469, App
302	71	77.2	42	4	US-10-279-061-84	Sequence 84, Appl	375	66	71.7	21	6	US-11-066-697-470	Sequence 470, App
303	71	77.2	56	6	US-11-066-697-489	Sequence 489, App	376	66	71.7	24	3	US-09-752-724-5	Sequence 5, Appl
304	71	77.2	126	4	US-10-419-059-3	Sequence 3, Appl	377	66	71.7	24	6	US-11-066-697-468	Sequence 468, App
305	71	77.2	126	4	US-10-645-874-3	Sequence 3, Appl	378	66	71.7	30	6	US-11-066-697-471	Sequence 471, App
306	71	77.2	126	5	US-10-827-919-3	Sequence 3, Appl	379	66	71.7	34	6	US-11-066-697-472	Sequence 472, App
307	71	77.2	131	4	US-10-279-061-88	Sequence 88, Appl	380	65	70.7	17	4	US-10-664-605-6	Sequence 6, Appl
308	71	77.2	151	4	US-10-419-059-4	Sequence 4, Appl	381	65	70.7	17	4	US-10-664-605-7	Sequence 7, Appl
309	71	77.2	151	4	US-10-645-874-4	Sequence 4, Appl	382	65	70.7	17	4	US-10-664-605-34	Sequence 34, Appl
310	71	77.2	151	5	US-10-827-919-4	Sequence 4, Appl	383	65	70.7	17	4	US-10-664-605-64	Sequence 64, Appl
311	71	77.2	153	4	US-10-201-288-17	Sequence 17, Appl	384	65	70.7	17	4	US-10-723-933-78	Sequence 78, Appl
312	71	77.2	153	5	US-10-919-325-6	Sequence 6, Appl	385	65	70.7	28	4	US-10-723-933-78	Sequence 78, Appl
313	71	77.2	161	3	US-09-864-408A-4402	Sequence 4402, Ap	386	65	70.7	28	5	US-11-040-810-7	Sequence 7, Appl
314	70	76.1	17	4	US-10-664-605-45	Sequence 45, Appl	387	65	70.7	28	6	US-11-040-810-7	Sequence 7, Appl
315	70	76.1	17	4	US-10-664-605-49	Sequence 49, Appl	388	65	70.7	35	6	US-11-066-697-506	Sequence 506, App
316	70	76.1	17	4	US-10-664-605-54	Sequence 54, Appl	389	65	70.7	45	6	US-11-066-697-510	Sequence 510, App
317	70	76.1	17	4	US-10-664-605-56	Sequence 56, Appl	390	64	69.6	17	4	US-10-664-605-38	Sequence 38, Appl
318	70	76.1	17	4	US-10-664-605-57	Sequence 57, Appl	391	64	69.6	17	4	US-10-664-605-39	Sequence 39, Appl
319	70	76.1	17	4	US-10-723-933-2	Sequence 2, Appl	392	64	69.6	21	3	US-09-466-268B-8	Sequence 8, Appl

393	64	69.6	28	5	US-10-471-348-19	Sequence 19, Appl	466	40	43.5	104	4	US-10-425-115-212795	Sequence 212795,
394	64	69.6	28	5	US-10-471-348-20	Sequence 20, Appl	467	40	43.5	105	4	US-10-437-963-111441	Sequence 111441,
395	64	69.6	28	6	US-11-040-810-19	Sequence 20, Appl	468	40	43.5	106	4	US-10-437-963-147758	Sequence 147758,
396	64	69.6	28	6	US-11-040-810-20	Sequence 20, Appl	469	40	43.5	117	4	US-10-437-963-169662	Sequence 169662,
397	63	68.5	17	4	US-10-327-514-18	Sequence 19, Appl	470	40	43.5	153	4	US-10-424-599-178803	Sequence 178803,
398	63	68.5	17	4	US-10-664-605-59	Sequence 58, Appl	471	40	43.5	154	4	US-10-424-599-178803	Sequence 178803,
399	63	68.5	17	5	US-10-499-762-18	Sequence 18, Appl	472	40	43.5	160	4	US-10-425-115-197466	Sequence 197466,
400	63	68.5	23	4	US-10-106-806-11	Sequence 11, Appl	473	40	43.5	230	4	US-10-424-599-190579	Sequence 190579,
401	63	68.5	23	5	US-10-947-730-11	Sequence 11, Appl	474	40	43.5	240	4	US-10-425-115-351233	Sequence 351233,
402	63	68.5	32	6	US-11-066-697-513	Sequence 513, Appl	475	40	43.5	264	4	US-10-437-963-111894	Sequence 111894,
403	63	68.5	38	3	US-09-466-2688-10	Sequence 10, Appl	476	40	43.5	264	4	US-10-369-493-4581	Sequence 4581, Ap
404	63	68.5	38	4	US-10-106-806-10	Sequence 10, Appl	477	40	43.5	396	4	US-10-282-122A-50952	Sequence 50952, A
405	63	68.5	38	5	US-10-947-730-10	Sequence 10, Appl	478	40	43.5	399	4	US-10-156-761-8126	Sequence 8126, Ap
406	63	68.5	45	3	US-09-752-724-7	Sequence 7, Appl	479	40	43.5	593	4	US-10-695-499-64	Sequence 64, Appl
407	63	68.5	45	6	US-11-066-697-514	Sequence 514, Appl	480	40	43.5	683	4	US-10-369-493-2188	Sequence 2188, Ap
408	62	67.4	22	6	US-10-471-348-18	Sequence 18, Appl	481	40	43.5	788	6	US-11-097-143-13725	Sequence 13725, A
409	62	67.4	22	6	US-11-040-810-18	Sequence 18, Appl	482	40	43.5	1001	5	US-10-745-237-2	Sequence 2, Appl
410	61	66.3	28	4	US-10-723-933-41	Sequence 41, Appl	483	40	43.5	1001	5	US-10-745-237-6	Sequence 8, Appl
411	61	66.3	28	5	US-10-471-348-11	Sequence 11, Appl	484	40	43.5	1287	6	US-11-097-143-12003	Sequence 12003, A
412	61	66.3	28	6	US-11-040-810-11	Sequence 11, Appl	485	40	43.5	2703	4	US-10-282-122A-66108	Sequence 66108, A
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415	58	63.0	22	6	US-11-040-810-14	Sequence 14, Appl	488	40	43.5	4899	5	US-10-450-763-42673	Sequence 42673, A
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417	58	63.0	28	4	US-10-723-933-135	Sequence 135, Appl	490	40	43.5	73	4	US-10-424-599-228439	Sequence 228439,
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422	54	58.7	42	3	US-09-466-2688-11	Sequence 11, Appl	495	39.5	42.9	91	4	US-10-425-115-349683	Sequence 349683,
423	52	56.5	18	3	US-09-027-777B-9	Sequence 9, Appl	496	39.5	42.9	124	5	US-10-684-422-126	Sequence 126, App
424	52	56.5	21	6	US-11-066-697-496	Sequence 496, Appl	497	39.5	42.9	171	4	US-10-437-963-102867	Sequence 102867,
425	50	54.3	17	4	US-10-664-605-5	Sequence 5, Appl	498	39	42.4	246	5	US-10-369-493-14229	Sequence 37, Appl
426	49	53.3	17	6	US-11-066-697-494	Sequence 494, Appl	499	39	42.4	262	5	US-10-822-613-37	Sequence 11454, A
427	48	52.2	14	4	US-10-664-605-14	Sequence 14, Appl	500	39	42.4	263	4	US-10-369-493-14635	Sequence 14635, A
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431	45	48.9	12	4	US-10-664-605-21	Sequence 21, Appl	504	39	42.4	444	4	US-10-369-493-6962	Sequence 6962, Ap
432	45	48.9	13	4	US-10-664-605-16	Sequence 16, Appl	505	39	42.4	597	3	US-09-793-306-146	Sequence 146, App
433	45	48.9	13	4	US-10-664-605-18	Sequence 18, Appl	506	39	42.4	611	4	US-10-282-122A-51459	Sequence 51459, A
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440	42	45.7	406	4	US-10-425-115-210308	Sequence 210308,	513	39	42.4	1245	4	US-10-153-668-176	Sequence 176, App
441	42	45.7	13	4	US-10-664-605-17	Sequence 17, Appl	514	39	42.4	1359	5	US-10-732-923-8889	Sequence 8889, Ap
442	42	45.7	13	4	US-10-664-605-19	Sequence 19, Appl	515	39	42.4	1385	5	US-10-732-923-8879	Sequence 8879, Ap
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446	42	45.7	237	4	US-10-335-977-6441	Sequence 6441, Ap	519	39	42.4	128	4	US-10-425-114-50807	Sequence 50807, A
447	42	45.7	237	4	US-10-335-977-6442	Sequence 6440, Ap	520	39	42.4	327	4	US-10-437-963-133368	Sequence 133368,
448	42	45.7	273	4	US-10-335-977-6443	Sequence 6442, Ap	521	39	42.4	336	5	US-10-739-930-9292	Sequence 9292, Ap
449	42	45.7	326	3	US-09-943-002-8	Sequence 8, Appl	522	39	42.4	555	4	US-10-437-963-198239	Sequence 198239,
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451	42	45.7	1518	5	US-10-450-763-53038	Sequence 53038, A	524	39	42.4	2296	5	US-10-952-915-27	Sequence 27, Appl
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453	41	44.6	72	4	US-10-425-115-327432	Sequence 327432,	526	39	42.4	54	4	US-11-066-697-493	Sequence 232531,
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455	41	44.6	307	3	US-09-738-973-397	Sequence 397, Appl	528	39	42.4				
456	41	44.6	307	3	US-09-854-133-397	Sequence 397, Appl	529	39	42.4				
457	41	44.6	307	4	US-10-144-649A-397	Sequence 397, Appl	530	38.5	41.8				
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544	38	41.3	144	3	US-09-822-827-480	Sequence 480, App	617	37	40.2	84	5	US-10-450-763-60380	Sequence 60380, A
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554	38	41.3	170	5	US-10-739-930-10278	Sequence 10278, A	627	37	40.2	126	4	US-10-425-115-203135	Sequence 203135, A
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562	38	41.3	235	4	US-10-767-701-38475	Sequence 38475, A	635	37	40.2	162	4	US-10-425-115-291927	Sequence 291927, A
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568	38	41.3	323	4	US-10-282-122A-47384	Sequence 47384, A	641	37	40.2	214	3	US-09-305-736-354	Sequence 354, App
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571	38	41.3	356	4	US-10-263-929-164	Sequence 164, App	644	37	40.2	214	3	US-10-621-401-354	Sequence 354, App
572	38	41.3	356	4	US-10-263-929-168	Sequence 168, App	645	37	40.2	226	4	US-10-296-115-980	Sequence 980, App
573	38	41.3	356	5	US-10-486-865-2	Sequence 2, Appli	646	37	40.2	241	4	US-10-360-101-223	Sequence 223, App
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577	38	41.3	491	4	US-10-437-963-113247	Sequence 113247, A	650	37	40.2	260	4	US-10-058-270A-134	Sequence 134, App
578	38	41.3	502	3	US-09-815-242-5904	Sequence 5904, Ap	651	37	40.2	260	5	US-10-936-626-94	Sequence 94, Appl
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582	38	41.3	560	3	US-09-815-242-13057	Sequence 13057, A	655	37	40.2	267	4	US-10-126-845-57	Sequence 57, Appl
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584	38	41.3	735	6	US-11-097-143-25491	Sequence 25491, A	657	37	40.2	267	5	US-10-955-656-57	Sequence 57, Appl
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586	38	41.3	803	4	US-10-369-493-1441	Sequence 1441, Ap	659	37	40.2	267	5	US-10-775-204-2220	Sequence 2220, Ap
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593	38	41.3	1260	4	US-10-437-963-152330	Sequence 152330, A	666	37	40.2	338	4	US-10-374-780A-1587	Sequence 1687, Ap
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881	37	40.2	513	4	US-10-063-580-124	Sequence 124, App	954	37	40.2	513	4	US-10-141-705-536	Sequence 536, App
882	37	40.2	513	4	US-10-011-692A-385	Sequence 385, App	955	37	40.2	513	4	US-10-141-753-536	Sequence 536, App
883	37	40.2	513	4	US-10-063-557-124	Sequence 124, App	956	37	40.2	513	4	US-10-141-758-536	Sequence 536, App
884	37	40.2	513	4	US-10-006-768A-385	Sequence 385, App	957	37	40.2	513	4	US-10-142-418-536	Sequence 536, App
885	37	40.2	513	4	US-10-017-610A-385	Sequence 385, App	958	37	40.2	513	4	US-10-142-420-536	Sequence 536, App
886	37	40.2	513	4	US-10-006-063A-385	Sequence 385, App	959	37	40.2	513	4	US-10-142-422-536	Sequence 536, App
887	37	40.2	513	4	US-10-063-585-124	Sequence 124, App	960	37	40.2	513	4	US-10-142-427-536	Sequence 536, App
888	37	40.2	513	4	US-10-020-063A-385	Sequence 385, App	961	37	40.2	513	4	US-10-142-760-536	Sequence 536, App
889	37	40.2	513	4	US-10-127-847A-536	Sequence 536, App	962	37	40.2	513	4	US-10-145-821-536	Sequence 536, App
890	37	40.2	513	4	US-10-015-391A-385	Sequence 385, App	963	37	40.2	513	4	US-10-152-531-536	Sequence 385, App
891	37	40.2	513	4	US-10-081-872-146	Sequence 146, App	964	37	40.2	513	4	US-10-006-172A-385	Sequence 385, App
892	37	40.2	513	4	US-10-017-407A-385	Sequence 385, App	965	37	40.2	513	4	US-10-127-840A-536	Sequence 536, App
893	37	40.2	513	4	US-10-011-833A-385	Sequence 385, App	966	37	40.2	513	4	US-10-142-424-536	Sequence 536, App
894	37	40.2	513	4	US-10-137-866-536	Sequence 536, App	967	37	40.2	513	4	US-10-142-761-536	Sequence 536, App
895	37	40.2	513	4	US-10-146-726-536	Sequence 536, App	968	37	40.2	513	4	US-10-142-763-536	Sequence 536, App
896	37	40.2	513	4	US-10-146-727-536	Sequence 536, App	969	37	40.2	513	4	US-10-142-765-536	Sequence 536, App
897	37	40.2	513	4	US-10-146-788-536	Sequence 536, App	970	37	40.2	513	4	US-10-142-887-536	Sequence 536, App
898	37	40.2	513	4	US-10-152-380-536	Sequence 536, App	971	37	40.2	513	4	US-10-142-888-536	Sequence 536, App
899	37	40.2	513	4	US-10-153-934-536	Sequence 536, App	972	37	40.2	513	4	US-10-143-034-536	Sequence 536, App
900	37	40.2	513	4	US-10-063-588-124	Sequence 124, App	973	37	40.2	513	4	US-10-143-116-536	Sequence 536, App
901	37	40.2	513	4	US-10-006-041A-385	Sequence 385, App	974	37	40.2	513	4	US-10-144-957-536	Sequence 536, App
902	37	40.2	513	4	US-10-015-822A-385	Sequence 385, App	975	37	40.2	513	4	US-10-144-992-536	Sequence 536, App
903	37	40.2	513	4	US-10-140-807-536	Sequence 536, App	976	37	40.2	513	4	US-10-145-015-536	Sequence 536, App


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; APPLICANT: ConjuChem, Inc.
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 2710
; CURRENT APPLICATION NUMBER: US/10/471,348
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 44
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 1 to 17
; NAME/KEY: SITE
; LOCATION: 18
; OTHER INFORMATION: Xaa represents Lys(AEEA-MPA) -CONH2
; OTHER INFORMATION: Description of Sequence: synthetic peptide
US-10-471-348-44

Query Match          100.0%; Score 92; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   |||||
Db 1 CFGRKMDRISSSSGLGC 17

RESULT 5
US-11-040-810-44
; Sequence 44, Application US/11040810
; Publication No. US20050176641A1
; GENERAL INFORMATION:
; APPLICANT: BAKIS, Peter
; APPLICANT: BRIDON, Dominique P.
; APPLICANT: CARETTE, Julie
; APPLICANT: LECLAIRE, France
; APPLICANT: LEGER, Roger
; APPLICANT: ROBITAILLE, Martin
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 500862003401
; CURRENT APPLICATION NUMBER: US/11/040,810
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: US 10/471,348
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/CA03/01097
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 09/623,548
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13576
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/657/276
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 44
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 1 to 17
; NAME/KEY: SITE
```

```
; LOCATION: 18
; OTHER INFORMATION: Xaa represents Lys(AEEA-MPA) -CONH2
; FEATURE:
; OTHER INFORMATION: Description of Sequence: synthetic peptide
US-11-040-810-44

Query Match          100.0%; Score 92; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   |||||
Db 1 CFGRKMDRISSSSGLGC 17

RESULT 6
US-10-723-933-130
; Sequence 130, Application US/10723933
; Publication No. US20040203081A1
; GENERAL INFORMATION:
; APPLICANT: James, Kenneth D.
; APPLICANT: Rahdakrishnan, Balasingham
; APPLICANT: Walker, Navdeep B.
; APPLICANT: Miller, Mark A.
; APPLICANT: Ekwuribe, Nnochiri N.
; TITLE OF INVENTION: NATRIURETIC COMPOUNDS, CONJUGATES, AND USES THEREOF
; FILE REFERENCE: 9233.108
; CURRENT APPLICATION NUMBER: US/10/723,933
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/429,151
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Natriuretic peptide
US-10-723-933-130

Query Match          100.0%; Score 92; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
   |||||
Db 1 CFGRKMDRISSSSGLGC 17

RESULT 7
US-10-471-348-31
; Sequence 31, Application US/10471348
; Publication No. US20040266673A1
; GENERAL INFORMATION:
; APPLICANT: ConjuChem, Inc.
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 2710
; CURRENT APPLICATION NUMBER: US/10/471,348
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 31
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 1 to 17
; NAME/KEY: SITE
```

```

; NAME/KEY: AMIDATION
; LOCATION: 23
; OTHER INFORMATION: Xaa represents His-CONH2
; FEATURE:
; OTHER INFORMATION: Description of Sequence: synthetic peptide
US-10-471-348-31
; Query Match 100.0%; Score 92; DB 5; Length 23;
; Best Local Similarity 100.0%; Pred. No. 4.2e-08;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFGRKMDRISSSGLGC 17
Db 1 CFGRKMDRISSSGLGC 17

RESULT 8
US-11-040-810-31
; Sequence 31, Application US/11040810
; Publication No. US20050176641A1
; GENERAL INFORMATION:
; APPLICANT: BAKIS, Peter
; APPLICANT: BRIDON, Dominique P.
; APPLICANT: CARETTE, Julie
; APPLICANT: LECCLAIRE, France
; APPLICANT: LEGER, Roger
; APPLICANT: ROBITAILLE, Martin
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 500862003401
; CURRENT APPLICATION NUMBER: US/11/040,810
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: US 10/471,348
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/CA03/01097
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 09/623,548
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13576
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/657/276
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 31
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 1 to 17
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 23
; OTHER INFORMATION: Xaa represents His-CONH2
; OTHER INFORMATION: Description of Sequence: synthetic peptide
US-11-040-810-31

Query Match 100.0%; Score 92; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFGRKMDRISSSGLGC 17
Db 1 CFGRKMDRISSSGLGC 17

RESULT 9
US-10-723-933-127
; Sequence 127, Application US/10723933

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```

; Publication No. US20040203081A1
; GENERAL INFORMATION:
; APPLICANT: James, Kenneth D.
; APPLICANT: Randakrishnan, Balasingham
; APPLICANT: Malkar, Navdeep B.
; APPLICANT: Miller, Mark A.
; APPLICANT: Ekwuribe, Nnochiri N.
; TITLE OF INVENTION: NATRIURETIC COMPOUNDS, CONJUGATES, AND USES THEREOF
; FILE REFERENCE: 9233.108
; CURRENT APPLICATION NUMBER: US/10/723,933
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/429,151
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 127
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Natriuretic peptide
; NAME/KEY: DISULFID
; LOCATION: (8) .. (8)
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (24) .. (24)
; US-10-723-933-127

Query Match 100.0%; Score 92; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFGRKMDRISSSGLGC 17
Db 8 CFGRKMDRISSSGLGC 24

RESULT 10
US-10-471-348-33
; Sequence 33, Application US/10471348
; Publication No. US20040266673A1
; GENERAL INFORMATION:
; APPLICANT: ConjuChem, Inc.
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 2710
; CURRENT APPLICATION NUMBER: US/10/471,348
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 33
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 1 to 17
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 24
; OTHER INFORMATION: Xaa represents Lys(AEEA-MPA)-CONH2
; OTHER INFORMATION: Description of Sequence: synthetic peptide
US-10-471-348-33

Query Match 100.0%; Score 92; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFGRKMDRISSSGLGC 17

```

Db 1 CFCGRKMDRISSSSGLGC 17
|||||

RESULT 11
US-11-040-810-33
; Sequence 33, Application US/11040810
; Publication No. US20050176641A1
; GENERAL INFORMATION:
; APPLICANT: BAKIS, Peter
; APPLICANT: BRIDON, Dominique P.
; APPLICANT: CARETTE, Julie
; APPLICANT: LECLAIRE, France
; APPLICANT: LEGER, Roger
; APPLICANT: ROBITAILLE, Martin
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 500862003401
; CURRENT APPLICATION NUMBER: US/11/040,810
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: US 10/471,348
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/CA03/01097
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 09/623,548
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13576
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/657/276
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 33
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 1 to 17
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 24
; OTHER INFORMATION: Xaa represents Lys(AEEA-MPA) -CONH2
; OTHER INFORMATION: Description of Sequence: synthetic peptide
US-11-040-810-33

Query Match 100.0%; Score 92; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFCGRKMDRISSSSGLGC 17
|||||

RESULT 12
US-11-040-810-33
; Sequence 22, Application US/10471348
; Publication No. US20040266673A1
; GENERAL INFORMATION:
; APPLICANT: ConjuChem, Inc.
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 2710
; CURRENT APPLICATION NUMBER: US/10/471,348
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 58

; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 3 to 19
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 25
; OTHER INFORMATION: Xaa represents His-CONH2
; OTHER INFORMATION: Description of Sequence: synthetic peptide
US-10-471-348-22

Query Match 100.0%; Score 92; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFCGRKMDRISSSSGLGC 17
|||||

Db 3 CFCGRKMDRISSSSGLGC 19
|||||

RESULT 13
US-10-471-348-24
; Sequence 24, Application US/10471348
; Publication No. US20040266673A1
; GENERAL INFORMATION:
; APPLICANT: ConjuChem, Inc.
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 2710
; CURRENT APPLICATION NUMBER: US/10/471,348
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 24
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 3 to 19
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 26
; OTHER INFORMATION: Xaa represents Lys(AEEA-MPA) -CONH2
; OTHER INFORMATION: Description of Sequence: synthetic peptide
US-10-471-348-24

Query Match 100.0%; Score 92; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFCGRKMDRISSSSGLGC 17
|||||

Db 3 CFCGRKMDRISSSSGLGC 19
|||||

RESULT 14
US-11-040-810-22
; Sequence 22, Application US/11040810
; Publication No. US20050176641A1
; GENERAL INFORMATION:
; APPLICANT: BAKIS, Peter
; APPLICANT: BRIDON, Dominique P.
; APPLICANT: CARETTE, Julie
; APPLICANT: LECLAIRE, France
; APPLICANT: LEGER, Roger

```
; APPLICANT: ROBITAILLE, Martin
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 500862003401
; CURRENT APPLICATION NUMBER: US/11/040,810
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: US 10/471,348
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/CA03/01097
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 09/623,548
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13576
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/657/276
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 22
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 3 to 19
; LOCATION: 25
; NAME/KEY: AMIDATION
; LOCATION: 25
; OTHER INFORMATION: Xaa represents His-CONH2
; FEATURE:
; OTHER INFORMATION: Description of Sequence: synthetic peptide
US-11-040-810-22

Query Match          100.0%; Score 92; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CFGRKMDRISSSSLGLC 17
Db      3  CFGRKMDRISSSSLGLC 19

RESULT 15
US-11-040-810-24
; Sequence 24, Application US/11040810
; Publication No. US20050176641A1
; GENERAL INFORMATION:
; APPLICANT: BAKIS, Peter
; APPLICANT: BRIDON, Dominique P.
; APPLICANT: CARETTE, Julie
; APPLICANT: LECLAIRE, France
; APPLICANT: LEGER, Roger
; APPLICANT: ROBITAILLE, Martin
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 500862003401
; CURRENT APPLICATION NUMBER: US/11/040,810
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: US 10/471,348
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/CA03/01097
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 09/623,548
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13576
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/657/276
; PRIOR FILING DATE: 2000-09-07
```

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; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 24
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 3 to 19
; LOCATION: 26
; NAME/KEY: SITE
; LOCATION: 26
; OTHER INFORMATION: Xaa represents Lys(AEEA-MPA)-CONH2
; FEATURE:
; OTHER INFORMATION: Description of Sequence: synthetic peptide
US-11-040-810-24

Query Match          100.0%; Score 92; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CFGRKMDRISSSSLGLC 17
Db      3  CFGRKMDRISSSSLGLC 19

RESULT 16
US-09-902-517-1
; Sequence 1, Application US/09902517
; Publication No. US20030109430A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOCASSAYS FOR HUMAN AND CANINE BRAIN
; TITLE OF INVENTION: NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A portion of human ANP and pBNP.
US-09-902-517-1

Query Match          100.0%; Score 92; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CFGRKMDRISSSSLGLC 17
Db      4  CFGRKMDRISSSSLGLC 20

RESULT 17
US-10-106-806-7
; Sequence 7, Application US/10106806
```

RESULT 19

RESULT 21
US-10-947-730-7
; Sequence 7, Application US/10947730
; Publication No. US20050059600A1
; GENERAL INFORMATION:
; APPLICANT: Burnett, Jr., John C.
; APPLICANT: Lisy, Ondrej
; TITLE OF INVENTION: Chimeric natriuretic peptides
; FILE REFERENCE: 150.199US2
; CURRENT APPLICATION NUMBER: US/10/947,730
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US/10/106,806
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 09/466,268
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-730-7

Query Match 100.0%; Score 92; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | |
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 22
US-10-723-933-106
; Sequence 106, Application US/10723933
; Publication No. US20040203081A1
; GENERAL INFORMATION:
; APPLICANT: James, Kenneth D.
; APPLICANT: Rahdakrishnan, Balasingham
; APPLICANT: Malkar, Navdeep B.
; APPLICANT: Miller, Mark A.
; APPLICANT: Ekwuribe, Nnochiri N.
; TITLE OF INVENTION: NATRIURETIC COMPOUNDS, CONJUGATES, AND USES THEREOF
; FILE REFERENCE: 9233.108
; CURRENT APPLICATION NUMBER: US/10/723,933
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/429,151
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Natriuretic peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)-(3)
; OTHER INFORMATION: Xaa is not Lys
US-10-723-933-106

Query Match 100.0%; Score 92; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | |
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 23
US-10-723-933-123

; Sequence 123, Application US/10723933
; Publication No. US20040203081A1
; GENERAL INFORMATION:
; APPLICANT: James, Kenneth D.
; APPLICANT: Rahdakrishnan, Balasingham
; APPLICANT: Malkar, Navdeep B.
; APPLICANT: Miller, Mark A.
; APPLICANT: Ekwuribe, Nnochiri N.
; TITLE OF INVENTION: NATRIURETIC COMPOUNDS, CONJUGATES, AND USES THEREOF
; FILE REFERENCE: 9233.108
; CURRENT APPLICATION NUMBER: US/10/723,933
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/429,151
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Natriuretic peptide
US-10-723-933-123

Query Match 100.0%; Score 92; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | |
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 24
US-09-752-724-4
; Sequence 4, Application US/09752724
; Patent No. US20010027181A1
; GENERAL INFORMATION:
; APPLICANT: KITAKAZE, Masafumi
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR USE IN TREATMENT OR PROPHYLAXIS
; TITLE OF INVENTION: ISCHEMIC HEART DISEASE
; FILE REFERENCE: JP/S-38-252US
; CURRENT APPLICATION NUMBER: US/09/752,724
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: JP 98134/2000
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-752-724-4

Query Match 100.0%; Score 92; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CFGRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | |
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 25
US-09-466-268B-6
; Sequence 6, Application US/09466268B
; Publication No. US20020082219A1
; GENERAL INFORMATION:
; APPLICANT: Burnett, Jr., John C.
; APPLICANT: Lisy, Ondrej
; TITLE OF INVENTION: Chimeric natriuretic peptides
; FILE REFERENCE: 150.199US1
; CURRENT APPLICATION NUMBER: US/09/466,268B

; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-466-268B-6

Query Match 100.0%; Score 92; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFCRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | |
DB 10 CFCRKMDRISSSSGLGC 26

RESULT 26

US-09-902-517-49
; Sequence 49, Application US/09902517
; Publication No. US20030109430A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
; TITLE OF INVENTION: NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: R2
US-09-902-517-49

Query Match 100.0%; Score 92; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFCRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | |
DB 10 CFCRKMDRISSSSGLGC 26

RESULT 27

US-10-106-806-6
; Sequence 6, Application US/10106806
; Publication No. US20030069186A1
; GENERAL INFORMATION:
; APPLICANT: Burnett, Jr., John C.
; APPLICANT: Lisy, Ondrej
; TITLE OF INVENTION: Chimeric natriuretic peptides
; FILE REFERENCE: 150.199US2
; CURRENT APPLICATION NUMBER: US/10/106,806

; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 09/466,268
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-806-6

Query Match 100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFCRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | |
DB 10 CFCRKMDRISSSSGLGC 26

RESULT 28

US-10-197-954-24
; Sequence 24, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqi, Suhaib
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-24

Query Match 100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFCRKMDRISSSSGLGC 17
| | | | | | | | | | | | | | | | | | | |
DB 10 CFCRKMDRISSSSGLGC 26

RESULT 29

US-10-402-021-49
; Sequence 49, Application US/10402021
; Publication No. US20040002458A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS USING NATRIURETIC PEPTID
; TITLE OF INVENTION: (AMENDED)
; FILE REFERENCE: 219002025203
; CURRENT APPLICATION NUMBER: US/10/402,021
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07

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; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: R2
US-10-402-021-49

```

```

Query Match      100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1  CFGRKMDRISSSSGLGC 17
      |||||
DB      10  CFGRKMDRISSSSGLGC 26

```

```

RESULT 30
US-10-664-605-4
; Sequence 4, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: ProChon Biotech Ltd.
; APPLICANT: Golemo, Myriam
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: P16860
; DATABASE ENTRY DATE: 2001-10-16
; RELEVANT RESIDUES: (103)..(134)
US-10-664-605-4

```

```

Query Match      100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  CFGRKMDRISSSSGLGC 17
      |||||
DB      10  CFGRKMDRISSSSGLGC 26

```

```

RESULT 31
US-10-723-933-33
; Sequence 33, Application US/10723933
; Publication No. US20040203081A1
; GENERAL INFORMATION:

```

```

; APPLICANT: James, Kenneth D.
; APPLICANT: Rahdakrishnan, Balasingham
; APPLICANT: Malkar, Navdeep B.
; APPLICANT: Miller, Mark A.
; APPLICANT: Ekwuribe, Nnochiri N.
; TITLE OF INVENTION: NATRIURETIC COMPOUNDS, CONJUGATES, AND USES THEREOF
; FILE REFERENCE: 9233.108
; CURRENT APPLICATION NUMBER: US/10/723,933
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/429,151
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Natriuretic peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Polypeptide may be present or absent
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)..(9)
; OTHER INFORMATION: Polypeptide may be present or absent
US-10-723-933-33

```

```

Query Match      100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  CFGRKMDRISSSSGLGC 17
      |||||
DB      10  CFGRKMDRISSSSGLGC 26

```

```

RESULT 32
US-10-723-933-53
; Sequence 53, Application US/10723933
; Publication No. US20040203081A1
; GENERAL INFORMATION:
; APPLICANT: James, Kenneth D.
; APPLICANT: Rahdakrishnan, Balasingham
; APPLICANT: Malkar, Navdeep B.
; APPLICANT: Miller, Mark A.
; APPLICANT: Ekwuribe, Nnochiri N.
; TITLE OF INVENTION: NATRIURETIC COMPOUNDS, CONJUGATES, AND USES THEREOF
; FILE REFERENCE: 9233.108
; CURRENT APPLICATION NUMBER: US/10/723,933
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/429,151
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Natriuretic peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Polypeptide may be present or absent
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)..(9)
; OTHER INFORMATION: Polypeptide may be present or absent
US-10-723-933-53

```

```

Query Match      100.0%; Score 92; DB 4; Length 32;

```



```
Best Local Similarity 100.0%; Pred. No. 5.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 33
US-10-723-933-73
; Sequence 73, Application US/10723933
; Publication No. US20040203081A1
; GENERAL INFORMATION:
; APPLICANT: James, Kenneth D.
; APPLICANT: Randakrishnan, Balasingham
; APPLICANT: Malkar, Navdeep B.
; APPLICANT: Miller, Mark A.
; APPLICANT: Ekwuribe, Nnochiri N.
; TITLE OF INVENTION: NATRIURETIC COMPOUNDS, CONJUGATES, AND USES THEREOF
; FILE REFERENCE: 9233.108
; CURRENT APPLICATION NUMBER: US/10/723,933
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/429,151
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (10)..(26)
; OTHER INFORMATION: Disulfide bond may be present or absent
US-10-723-933-73

Query Match 100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 34
US-10-723-933-110
; Sequence 110, Application US/10723933
; Publication No. US20040203081A1
; GENERAL INFORMATION:
; APPLICANT: James, Kenneth D.
; APPLICANT: Randakrishnan, Balasingham
; APPLICANT: Malkar, Navdeep B.
; APPLICANT: Miller, Mark A.
; APPLICANT: Ekwuribe, Nnochiri N.
; TITLE OF INVENTION: NATRIURETIC COMPOUNDS, CONJUGATES, AND USES THEREOF
; FILE REFERENCE: 9233.108
; CURRENT APPLICATION NUMBER: US/10/723,933
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/429,151
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 110
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Natriuretic peptide
; NAME/KEY: MISC_FEATURE
; LOCATION: (30)..(30)
; OTHER INFORMATION: Xaa is not Arg
US-10-723-933-110

Query Match 100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 35
US-10-723-933-111
; Sequence 111, Application US/10723933
; Publication No. US20040203081A1
; GENERAL INFORMATION:
; APPLICANT: James, Kenneth D.
; APPLICANT: Randakrishnan, Balasingham
; APPLICANT: Malkar, Navdeep B.
; APPLICANT: Miller, Mark A.
; APPLICANT: Ekwuribe, Nnochiri N.
; TITLE OF INVENTION: NATRIURETIC COMPOUNDS, CONJUGATES, AND USES THEREOF
; FILE REFERENCE: 9233.108
; CURRENT APPLICATION NUMBER: US/10/723,933
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/429,151
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Natriuretic peptide
; NAME/KEY: MISC_FEATURE
; LOCATION: (27)..(27)
; OTHER INFORMATION: Xaa is not Lys
US-10-723-933-111

Query Match 100.0%; Score 92; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 36
US-10-818-246-5
; Sequence 5, Application US/10818246
; Publication No. US20040249121A1
; GENERAL INFORMATION:
; APPLICANT: Novetide, Ltd.
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF CYCLIC PEPTIDES
; FILE REFERENCE: 12647/46002
; CURRENT APPLICATION NUMBER: US/10/818,246
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: 60/461,222
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-818-246-5

Query Match 100.0%; Score 92; DB 5; Length 32;
```

Best Local Similarity 100.0%; Pred. No. 5.9e-08; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 Db 10 CFGRKMDRISSSSGLGC 26

RESULT 37
 US-10-471-348-21
 ; Sequence 21, Application US/10471348
 ; Publication No. US20040266673A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ConjuChem, Inc.
 ; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
 ; FILE REFERENCE: 2710
 ; CURRENT APPLICATION NUMBER: US/10/471,348
 ; CURRENT FILING DATE: 2003-09-08
 ; PRIOR APPLICATION NUMBER: US 60/400,199
 ; PRIOR FILING DATE: 2002-07-31
 ; PRIOR APPLICATION NUMBER: US 60/400,413
 ; PRIOR FILING DATE: 2002-07-31
 ; NUMBER OF SEQ ID NOS: 58
 ; SEQ ID NO 21
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: DISULFID
 ; LOCATION: From 10 to 26
 ; NAME/KEY: AMIDATION
 ; LOCATION: 32
 ; OTHER INFORMATION: Xaa represents His-CONH2
 ; FEATURE:
 ; OTHER INFORMATION: Description of Sequence: synthetic peptide
 US-10-471-348-21

Query Match 100.0%; Score 92; DB 5; Length 32;
 Best Local Similarity 100.0%; Pred. No. 5.9e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 Db 10 CFGRKMDRISSSSGLGC 26

RESULT 38
 US-10-471-348-54
 ; Sequence 54, Application US/10471348
 ; Publication No. US20040266673A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ConjuChem, Inc.
 ; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
 ; FILE REFERENCE: 2710
 ; CURRENT APPLICATION NUMBER: US/10/471,348
 ; CURRENT FILING DATE: 2003-09-08
 ; PRIOR APPLICATION NUMBER: US 60/400,199
 ; PRIOR FILING DATE: 2002-07-31
 ; PRIOR APPLICATION NUMBER: US 60/400,413
 ; PRIOR FILING DATE: 2002-07-31
 ; NUMBER OF SEQ ID NOS: 58
 ; SEQ ID NO 54
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: DISULFID
 ; LOCATION: From 10 to 26
 ; NAME/KEY: SITE
 ; LOCATION: 1
 ; OTHER INFORMATION: Xaa represents MPA-AEEA-Ser

FEATURE:
 ; NAME/KEY: AMIDATION
 ; LOCATION: 32
 ; OTHER INFORMATION: Xaa represents His-CONH2
 ; FEATURE:
 ; OTHER INFORMATION: Description of Sequence: synthetic peptide
 US-10-471-348-54

Query Match 100.0%; Score 92; DB 5; Length 32;
 Best Local Similarity 100.0%; Pred. No. 5.9e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 Db 10 CFGRKMDRISSSSGLGC 26

RESULT 39
 US-10-760-085-24
 ; Sequence 24, Application US/10760085
 ; Publication No. US20050042771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hubert K"ster
 ; APPLICANT: Daniel Paul Little
 ; APPLICANT: Suhaib Mahmood Siddiqi
 ; APPLICANT: Matthew Peter Grealish
 ; APPLICANT: Subramaniam Marappan
 ; APPLICANT: Chester Frederick Haasman III
 ; APPLICANT: Ping Yip
 ; TITLE OF INVENTION: Capture Compounds, Collections Thereof
 ; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
 ; TITLE OF INVENTION: Compositions
 ; FILE REFERENCE: 24743-2309
 ; CURRENT APPLICATION NUMBER: US/10/760,085
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: 60/441,398
 ; PRIOR FILING DATE: 2003-01-16
 ; NUMBER OF SEQ ID NOS: 149
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-760-085-24

Query Match 100.0%; Score 92; DB 5; Length 32;
 Best Local Similarity 100.0%; Pred. No. 5.9e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
 Db 10 CFGRKMDRISSSSGLGC 26

RESULT 40
 US-10-947-730-6
 ; Sequence 6, Application US/10947730
 ; Publication No. US20050059600A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burnett, Jr., John C.
 ; APPLICANT: Liszy, Ondrej
 ; TITLE OF INVENTION: Chimeric natriuretic peptides
 ; FILE REFERENCE: 150.199US2
 ; CURRENT APPLICATION NUMBER: US/10/947,730
 ; CURRENT FILING DATE: 2004-09-23
 ; PRIOR APPLICATION NUMBER: US/10/106,806
 ; PRIOR FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: US 09/466,268
 ; PRIOR FILING DATE: 1999-12-17
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 32

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-730-6

Query Match      100.0%; Score 92; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 41
US-10-989-397-2
; Sequence 2, Application US/10989397
; Publication No. US20050089514A1
; GENERAL INFORMATION:
; APPLICANT: Forssmann, Wolf-Georg
; APPLICANT: Krause, Alexander
; APPLICANT: Maronde, Erik
; TITLE OF INVENTION: Use of Natriuretic Peptides as Antibiotically Active
; TITLE OF INVENTION: Substances for the Treatment of Bacterial Infections
; FILE REFERENCE: 020265us
; CURRENT APPLICATION NUMBER: US/10/989,397
; CURRENT FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US/10/069,128
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: DE19942230.3
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-989-397-2

Query Match      100.0%; Score 92; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 42
US-10-775-204-1802
; Sequence 1802, Application US/10775204
; Publication No. US20050186664A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-730-6

Query Match      100.0%; Score 92; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 43
US-11-040-810-21
; Sequence 21, Application US/11040810
; Publication No. US20050176641A1
; GENERAL INFORMATION:
; APPLICANT: BAKIS, Peter
; APPLICANT: BRIDON, Dominique P.
; APPLICANT: CARETTE, Julie
; APPLICANT: LECLAIRE, France
; APPLICANT: LEGER, Roger
; APPLICANT: ROBITAILLE, Martin
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 500862003401
; CURRENT APPLICATION NUMBER: US/11/040,810
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: US 10/471,348
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/CA03/01097
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 09/623,548
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13576
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/657/276
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 21
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 10 to 26
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 32
; OTHER INFORMATION: Xaa represents His-CONH2
; FEATURE:
; OTHER INFORMATION: Description of Sequence: synthetic peptide
US-11-040-810-21

Query Match      100.0%; Score 92; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 509
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-509

Query Match 100.0%; Score 92; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 46
US-11-066-697-516
; Sequence 516, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 516
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-516

Query Match 100.0%; Score 92; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

; APPLICANT: BAKIS, Peter
; APPLICANT: BRIDON, Dominique P.
; APPLICANT: CARETTE, Julie
; APPLICANT: LECLAIRE, France
; APPLICANT: LEGER, Roger
; APPLICANT: ROBITAILLE, Martin
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 500862003401
; CURRENT APPLICATION NUMBER: US/11/040,810
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: US 10/471,348
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/CA03/01097
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 09/623,548
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13576
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/657/276
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 54
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 10 to 26
; NAME/KEY: SITE
; LOCATION: 1
; OTHER INFORMATION: Xaa represents MPA-AEEA-Ser
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 32
; OTHER INFORMATION: Xaa represents His-CONH2
; FEATURE:
; OTHER INFORMATION: Description of Sequence: synthetic peptide
US-11-040-810-54

Query Match 100.0%; Score 92; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 1 CFGRKMDRISSSSGLGC 17
Db 10 CFGRKMDRISSSSGLGC 26

RESULT 45
US-11-066-697-509
; Sequence 509, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.

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; NAME/KEY: SITE
; LOCATION: (22)..(22)
; OTHER INFORMATION: side chain BzI modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (23)..(23)
; OTHER INFORMATION: side chain BzI modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (27)..(27)
; OTHER INFORMATION: side chain 4-CH3OBzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (28)..(28)
; OTHER INFORMATION: side chain Cl-Z modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (31)..(31)
; OTHER INFORMATION: side chain TOS modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (32)..(32)
; OTHER INFORMATION: side chain TOS modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (33)..(33)
; OTHER INFORMATION: side chain Bom modified
US-09-942-709-1

Query Match          100.0%; Score 92; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFGRKMDRISSSSGLGC 17
Db 11 CFGRKMDRISSSSGLGC 27

RESULT 48
US-10-723-933-112
; Sequence 112, Application US/10723933
; Publication No. US20040203081A1
; GENERAL INFORMATION:
; APPLICANT: James, Kenneth D.
; APPLICANT: Rahdakrishnan, Balasingham
; APPLICANT: Malkar, Navdeep B.
; APPLICANT: Miller, Mark A.
; APPLICANT: Ekwuribe, Nnochiri N.
; TITLE OF INVENTION: NATRIURETIC COMPOUNDS, CONJUGATES, AND USES THEREOF
; FILE REFERENCE: 9233.108
; CURRENT APPLICATION NUMBER: US/10/723,933
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/429,151
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 112
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Natriuretic peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (33)..(33)
; OTHER INFORMATION: Xaa may be Lys or Cys
US-10-723-933-112

Query Match          100.0%; Score 92; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFGRKMDRISSSSGLGC 17

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Db      |||||
10 CFGRKMDRISSSSGLGC 26

RESULT 49
US-10-697-886-1
; Sequence 1, Application US/10697886
; Publication No. US20040253655A1
; GENERAL INFORMATION:
; APPLICANT: TSUJI, Tetsuo
; APPLICANT: INOUE, Ken
; APPLICANT: YAMAUCHI, Akira
; APPLICANT: KONO, Masao
; APPLICANT: IGANO, Ken'ichi
; FILE REFERENCE: 0032-0262P
; CURRENT APPLICATION NUMBER: US/10/697,886
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US/09/942,709
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 3-326961
; PRIOR FILING DATE: 1991-11-14
; PRIOR APPLICATION NUMBER: US 07/976,457
; PRIOR FILING DATE: 1992-11-13
; PRIOR APPLICATION NUMBER: US 08/236,013
; PRIOR FILING DATE: 1994-05-02
; PRIOR APPLICATION NUMBER: US 08/749,031
; PRIOR FILING DATE: 1996-11-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amino acid according to the usual solid phase method
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal BOC modified side chain Br-Z modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)..(2)
; OTHER INFORMATION: side chain Bzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(4)
; OTHER INFORMATION: side chain Cl-Z modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)..(9)
; OTHER INFORMATION: side chain Bzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)..(11)
; OTHER INFORMATION: side chain 4-CH3OBzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (14)..(14)
; OTHER INFORMATION: side chain TOS modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (15)..(15)
; OTHER INFORMATION: side chain Cl-Z modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (17)..(17)
; OTHER INFORMATION: side chain OCHex modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)..(20)
; OTHER INFORMATION: side chain Bzl modified
; FEATURE:

; NAME/KEY: SITE
; LOCATION: (21)..(21)
; OTHER INFORMATION: side chain Bzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (22)..(22)
; OTHER INFORMATION: side chain Bzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (23)..(23)
; OTHER INFORMATION: side chain Bzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (27)..(27)
; OTHER INFORMATION: side chain 4-CH3OBzl modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (28)..(28)
; OTHER INFORMATION: side chain Cl-Z modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (31)..(31)
; OTHER INFORMATION: side chain TOS modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (32)..(32)
; OTHER INFORMATION: side chain TOS modified
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (33)..(33)
; OTHER INFORMATION: side chain Bom modified
; US-10-697-886-1

Query Match      100.0%; Score 92; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CFGRKMDRISSSSGLGC 17
Db      11 CFGRKMDRISSSSGLGC 27

RESULT 50
US-10-471-348-55
; Sequence 55, Application US/10471348
; Publication No. US20040266673A1
; GENERAL INFORMATION:
; APPLICANT: ConjuChem, Inc.
; TITLE OF INVENTION: Long lasting natriuretic peptide derivatives
; FILE REFERENCE: 2710
; CURRENT APPLICATION NUMBER: US/10/471,348
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: US 60/400,199
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/400,413
; PRIOR FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 55
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: From 10 to 26
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 33
; OTHER INFORMATION: Xaa represents Lys(AEEA-MPA)-CONH2
; FEATURE:
; OTHER INFORMATION: Description of Sequence: synthetic peptide
; US-10-471-348-55

Query Match      100.0%; Score 92; DB 5; Length 33;
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Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFGRKMDRISSSGLGC 17
| | | | | | | | | | | | | | | | |
Db 10 CFGRKMDRISSSGLGC 26

Search completed: January 25, 2006, 18:50:01
Job time : 77 secs

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